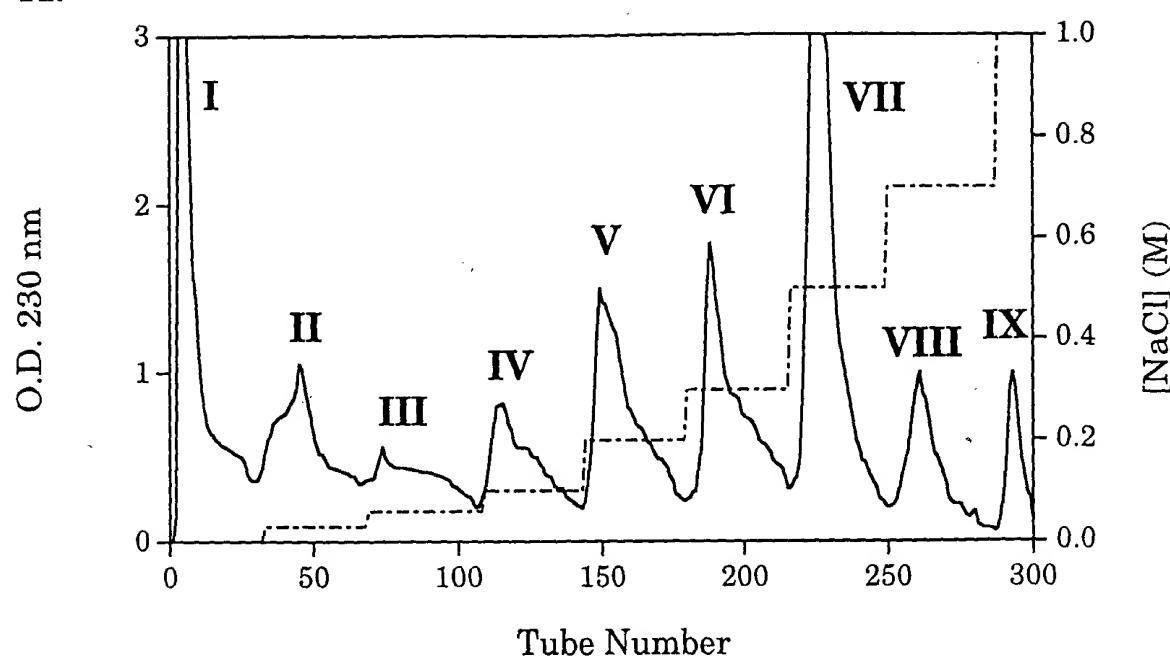


FIG 1.0

A.



B.

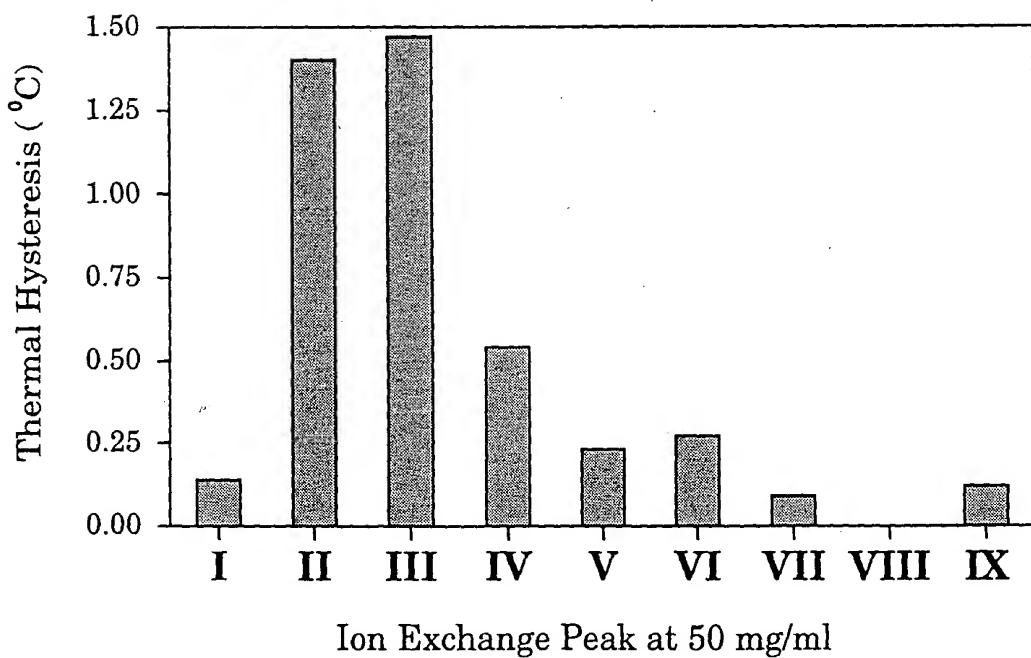


FIG 1.1

FIGURE 1.2

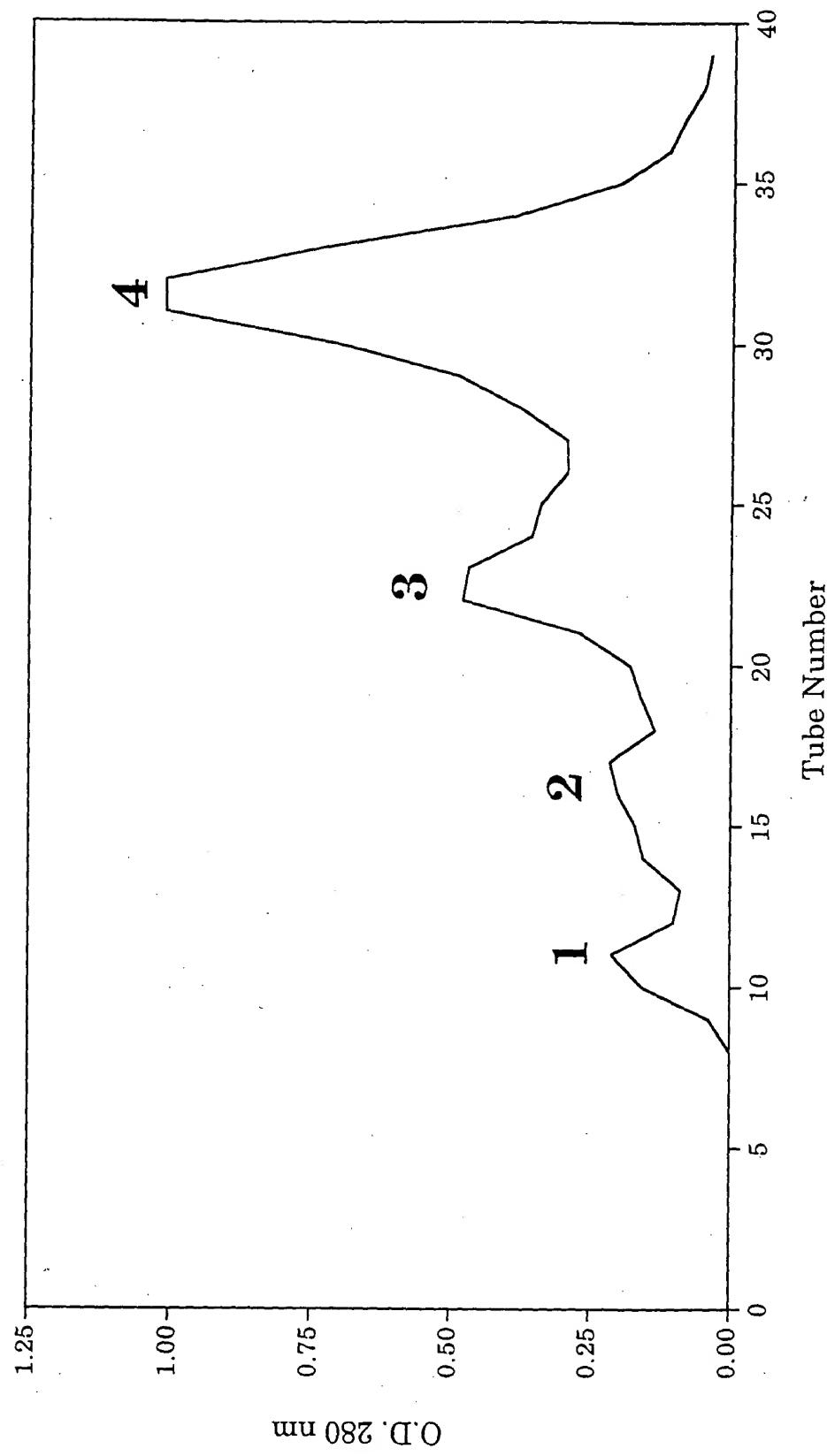


FIG 1.2

CONFIDENTIAL - DRAFT

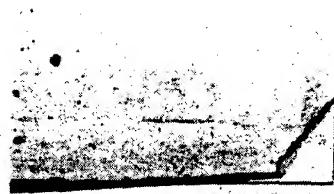


FIG 1.3

Tm-12.86►

12.5      25

FIG 1.4

000926266 "GEGE"

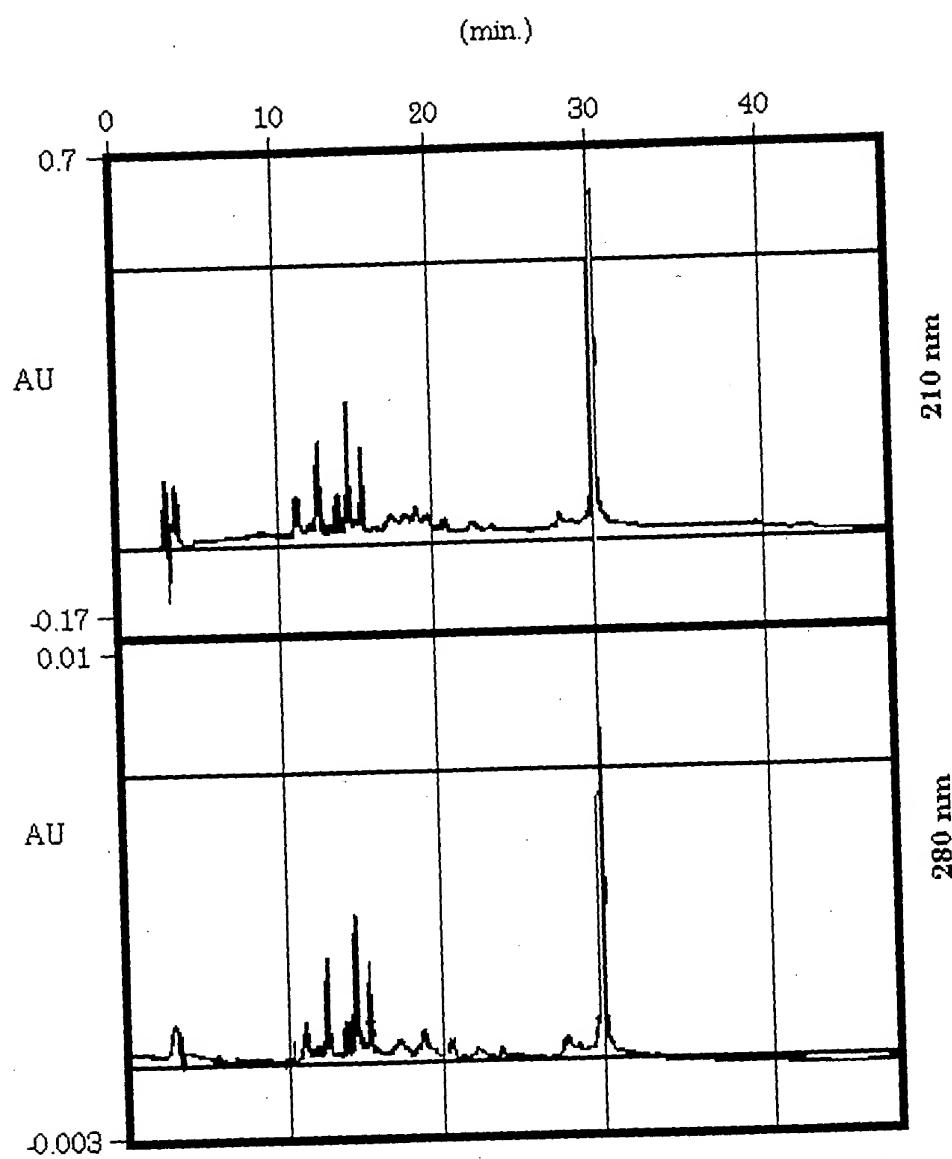


FIG. 1.5

0 0 0 0 0 0 0 0 0

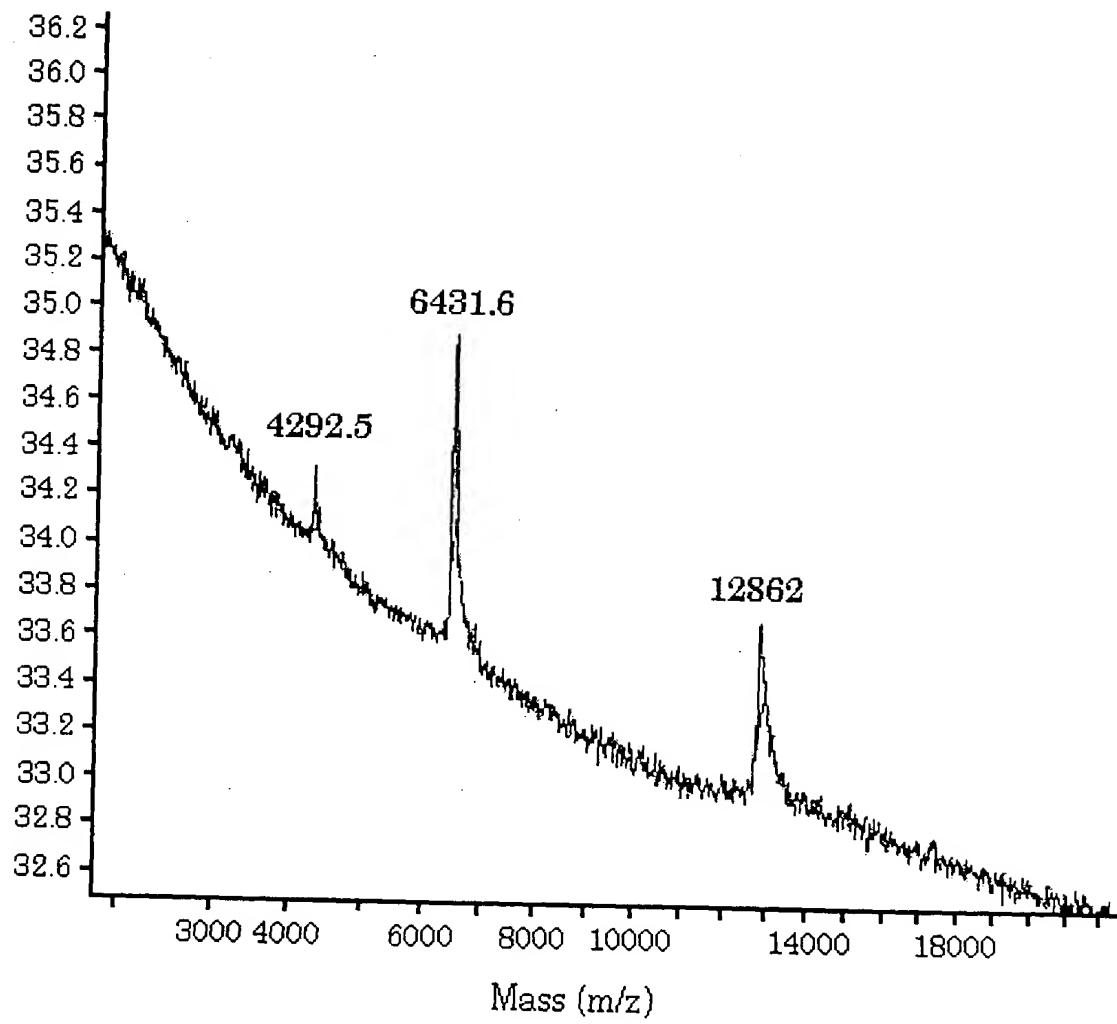


FIG 1.6

Y H E S G D G G

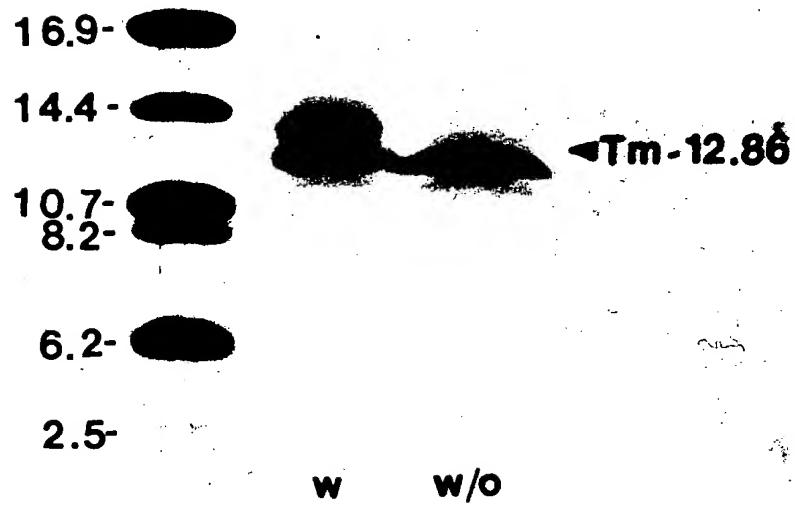


FIG 1.7

NH<sub>2</sub>-L-T-D-E-Q-I-Q-K-R-N-K-I-S-K-E-?-Q-Q-V  
Val  
Gln  
Gln  
Gln  
Glu  
Gln  
Gln  
Glu  
Lys  
Ser  
Ile  
Lys  
Asn  
Arg  
Arg  
Lys  
Gln  
Gln  
Ile  
Gln  
Glu  
Asp  
Thr  
Leu

FIG. 1.8

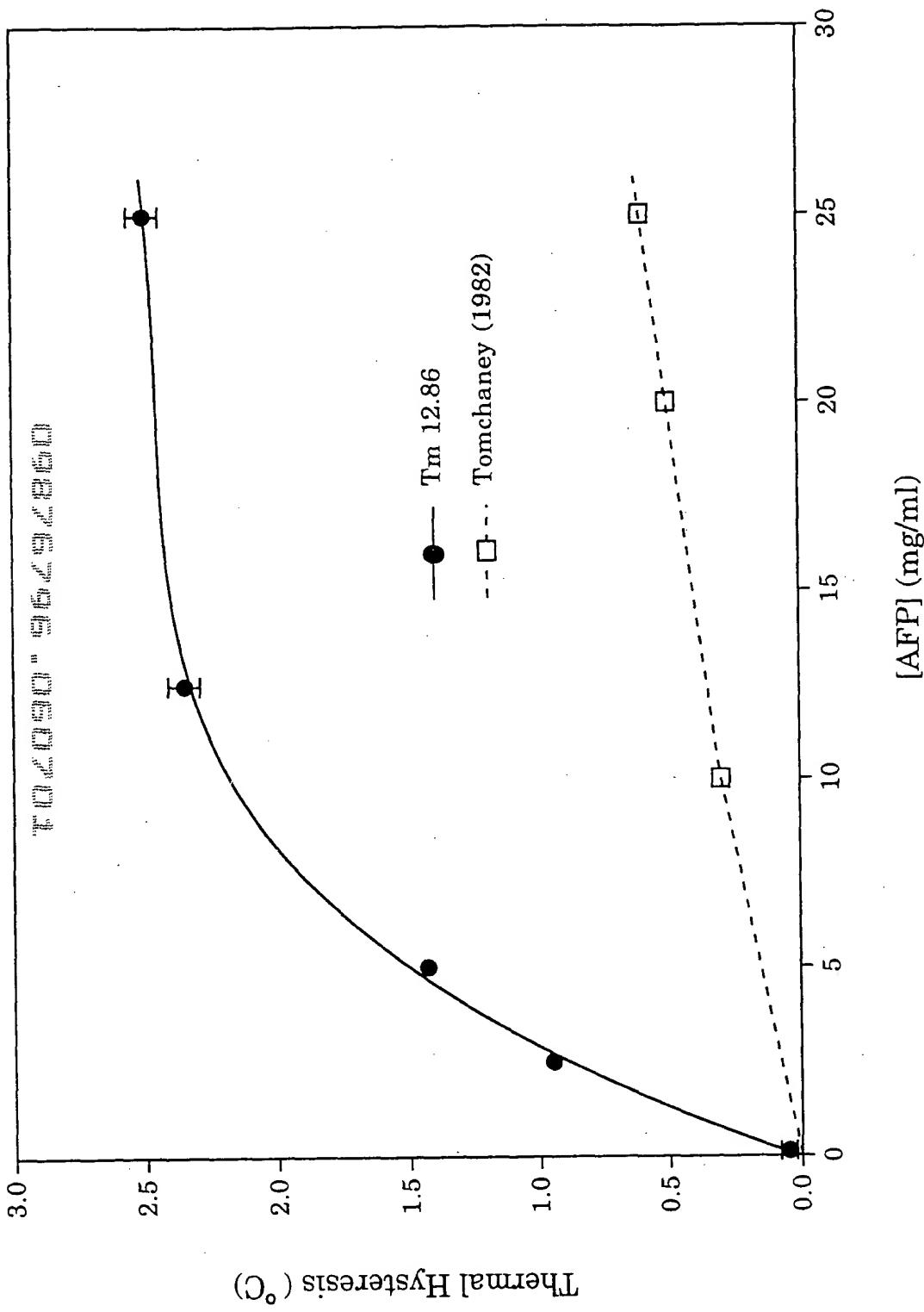


FIG 1.9

09376796 - 060204

1    2.5    5    10    15    20    M

-44.0

-32.3

-17.4

-7.8

FIG 1.10

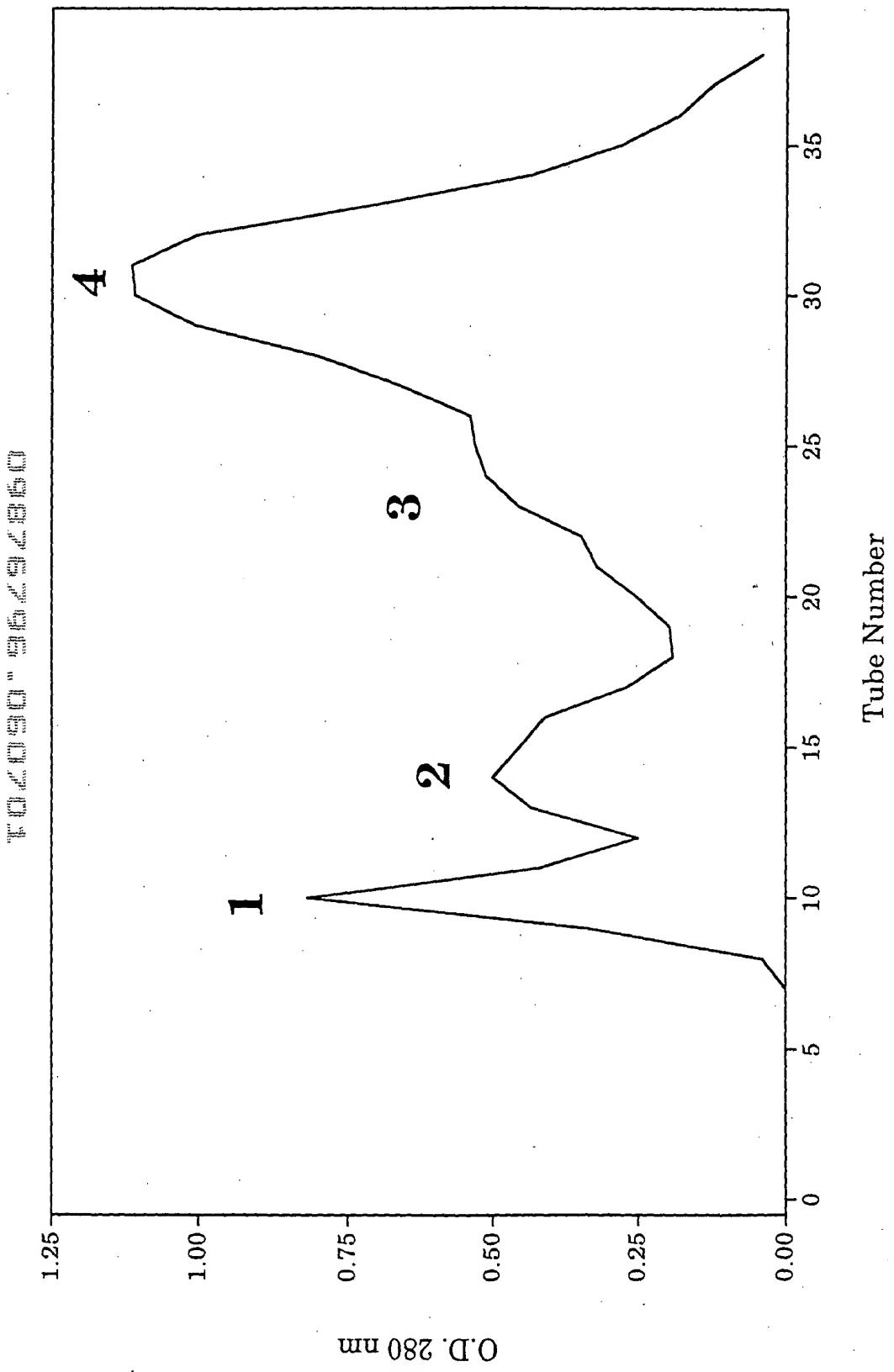


FIG 1.11

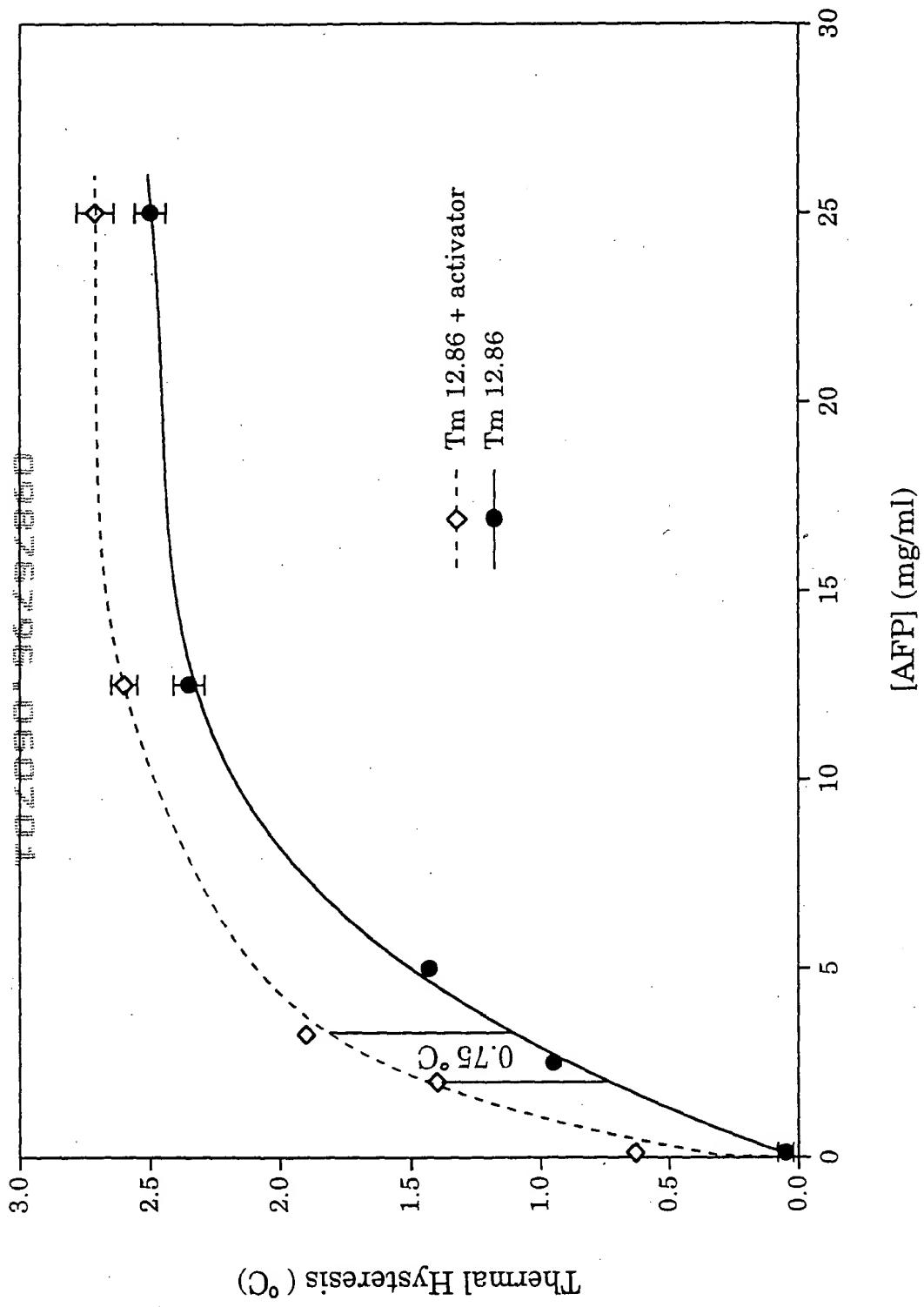


FIG 1.12

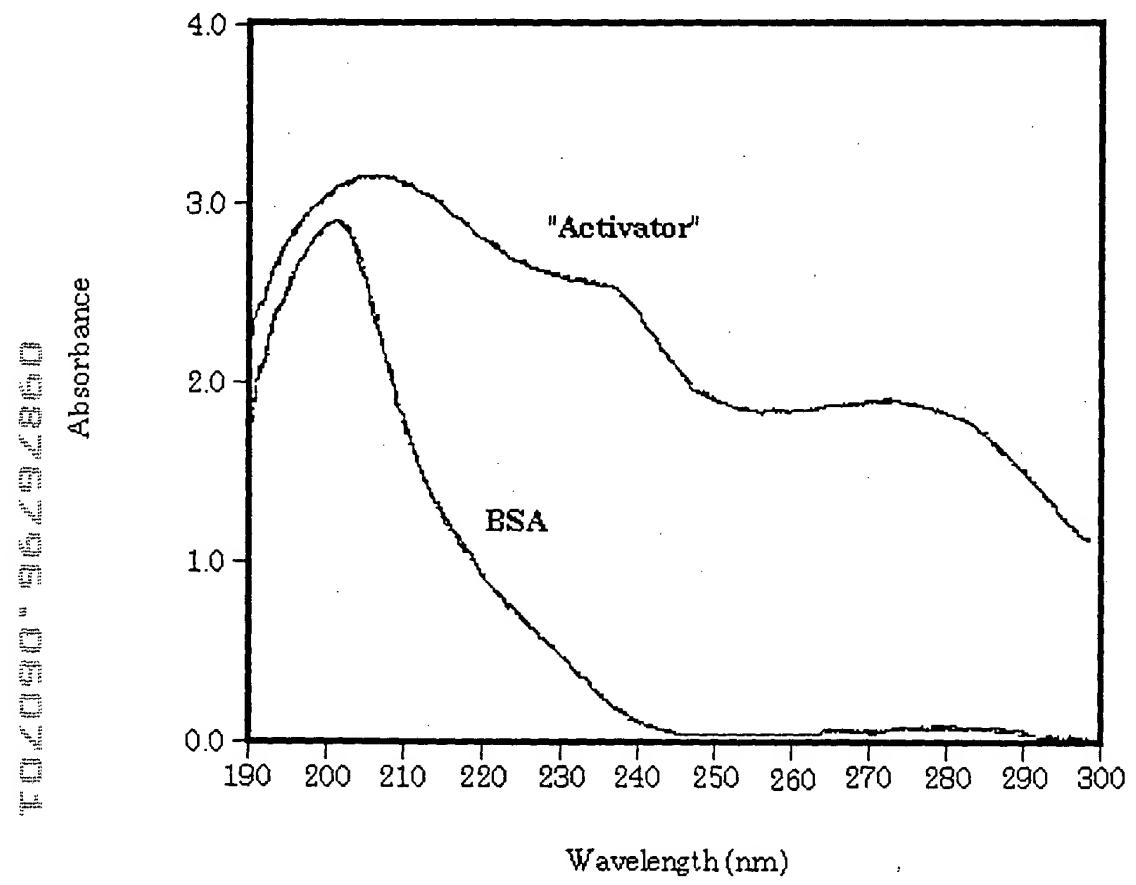


FIG. 1.13

0000000000000000

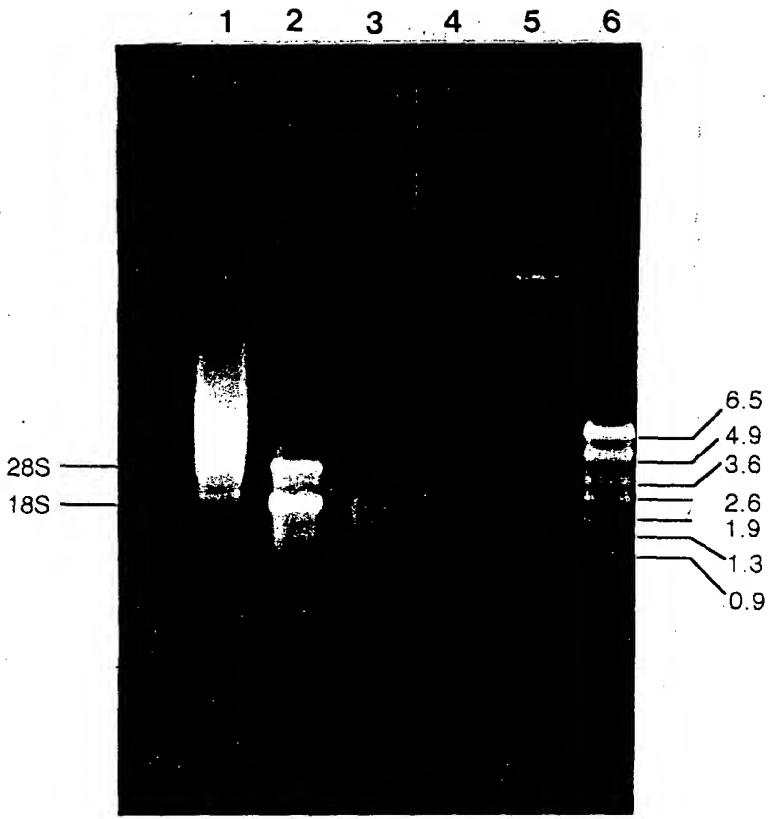


FIG 2.0

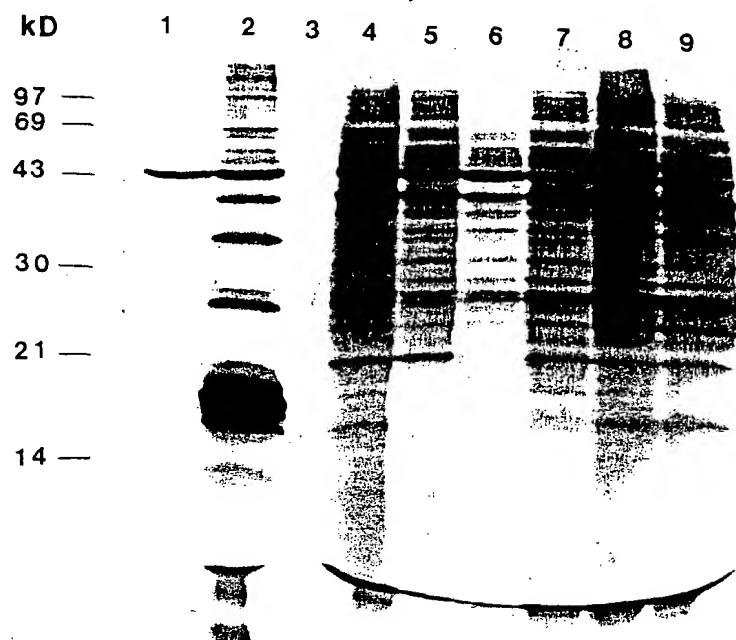


FIG 2.1

09376396 "062204

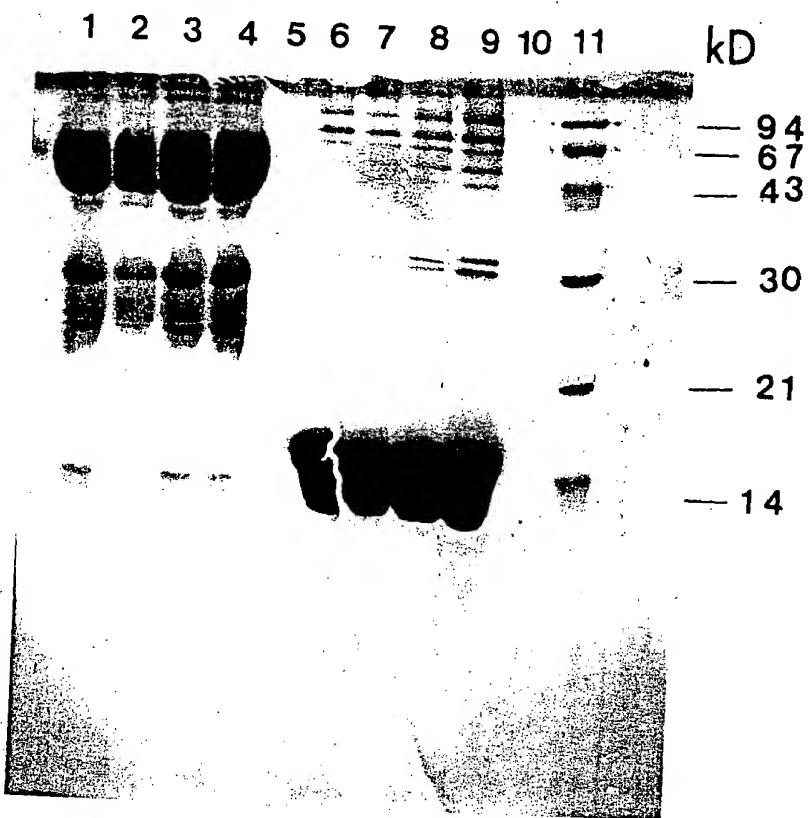


FIG 2.2

0 9 8 7 6 5 4 3 " C 2 1 0 2 0 1

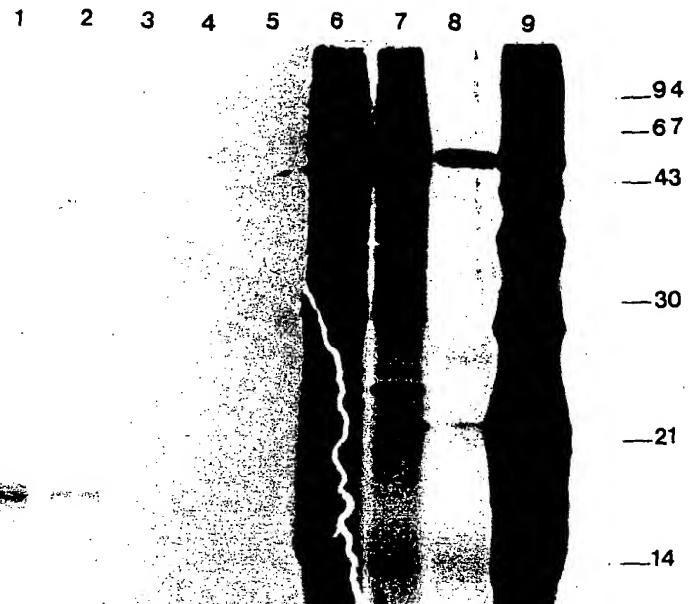


FIG 2.3

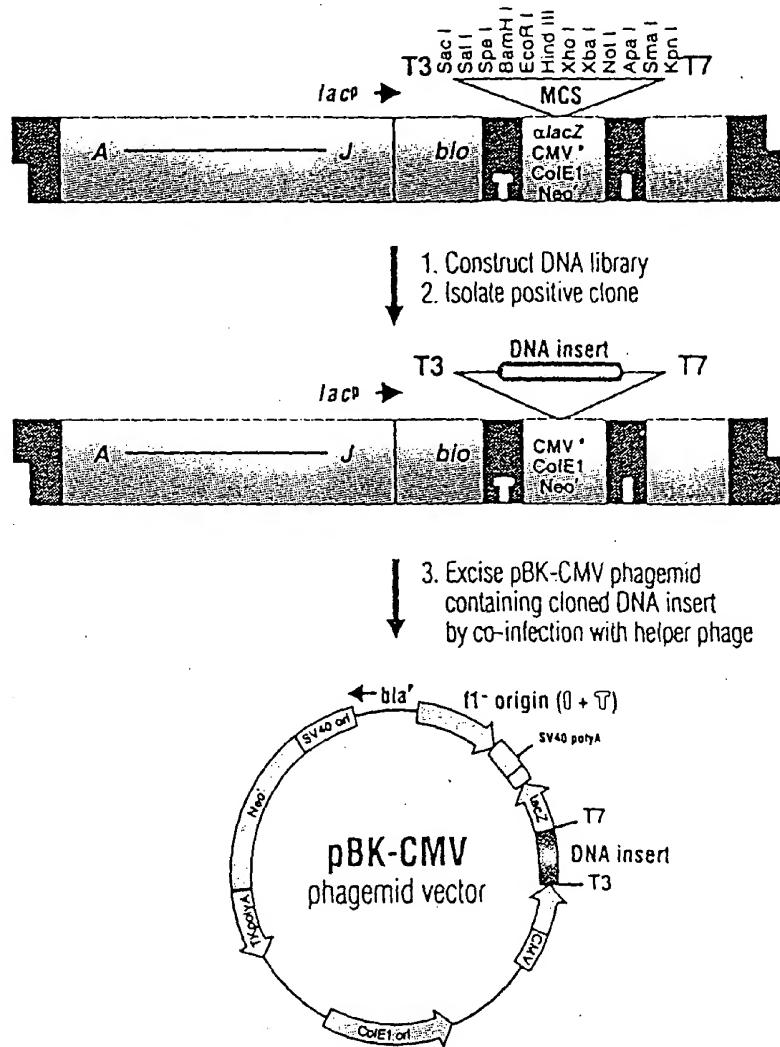
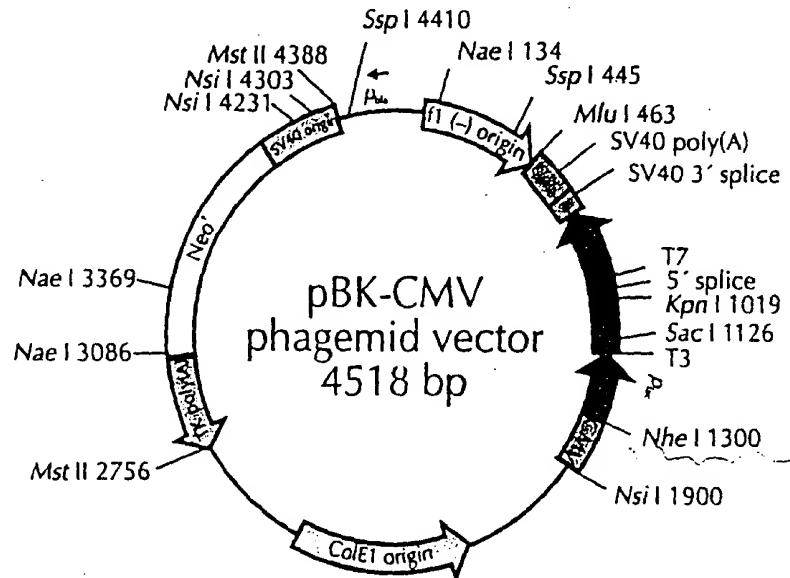


FIG. 2.4 a



BK Reverse Primer  
 $5'$  ACAGGAAACAGCTATGACCTTG  $3'$

T3 Primer  
 $5'$  ATTAAACCCCACTAAGGG  $3'$

1200 MET T3 promoter +1 → Sac I BspH II Sph I Sac I BpuMI Ecor I

$5'$  TCACACAGGAAACAGCTATGACCTTGAACTTAAACCCCAACTAAGGGAAACAAAAGCTGGAGETCGCGCGCTGCAGGTCCACACTAGTGGATCCAAG  
 $3'$  AGTGTGTCCTTTGATGATACTATGGGGTTGCCATTAAATGGGGATGATTTCCTTGCACCTCGACCCGGGGACGCTGCAGCTGTGATCACCTAGGTTCTAA

1183  $\beta$ -Galactosidase →

Xba I AspI/BpuMI BpuMI Kpn I

Hind III Sac I Xba I Not I Apa I Cla I Sma I Kpn I

ATTCCAAAAGCTCTCGAGAGTACTCTAGAGGGGGGGCCCATCGATTTCACCCGGGTGGGTACCGGTAAGTACCCAACTGGCCCTATAGTGAAGTCGATTACAATTCTACGGCCGCGTTTAC A  $3'$  (+)  
 GTTTTCAAGAGCTCTCATGAAGATCTCCCGGGGGGGTAGCTAAAAGGTGGCCACCCCATGGTCCATTCACTGGTTAACGGGATATCACTAACGATAATTGTTAAGTCGACCCGAGAAAATGT  $5'$  (-)

← +1 T7 promoter T7 Primer M13-20 Primer

FIG. 2.4 b

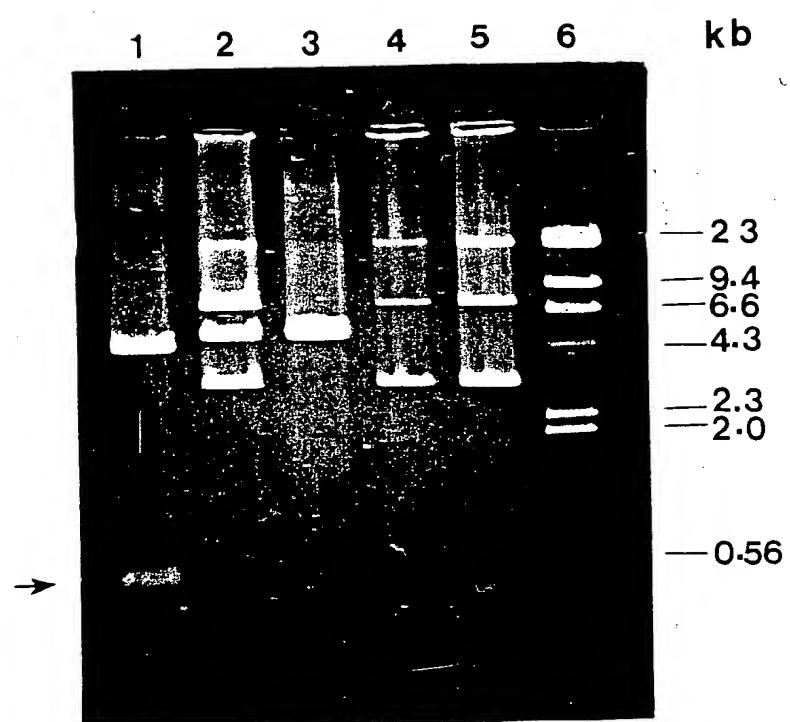


FIG. 2.5

DNA sequence of Tm 13.17 cDNA clone

B E  
a C  
m O  
H R  
I I

1 AGTGGATCCAAAGAATTGGCACGAGACTACTAACGATGAAGTTGCTCTGTTGTCTAATCT  
M K L L C C L I S

61 CCCTCATTCTGTTGGTCACAGTTCAGGCCCTGACCGAGGCACAAATTGAGAAACTGAACA  
L I L L V T V Q A L T E A Q I E K L N K

121 AGATCAGCAAAAATGTCAAATGAAAGTGGAGTGTCGCAAGAGATCATAACCAAAGCTC  
I S K K C Q N E S G V S Q E I I T K A R

181 GCAACGGTGACTGGGAGGACGATCCTAAACTGAAACGCCAAGTTTGCGTGGCCAGGA  
N G D W E D D P K L K R Q V F C V A R N

241 ACGCCGGTCTGGCCACGGAATCGGGAGAGGTGGTGGTGCACGTGTTGAGGGAGAAGGTGA  
A G L A T E S G E V V V D V L R E K V R

301 GGAAGGTCACTGACAACGACGAAGAAACTGAGAAAATCATCAATAAGTGCCCGTCAAGA  
K V T D N D E E T E K I I N K C A V K R

361 GAGATAACTGTTGAAGAGACGGTGTCAATACTTCAAATGTGTCATGAAAAACAAGCCAA  
D T V E E T V F N T F K C V M K N K P K

421 AGTTCTACCAGTGTGATTGAACCACACGACTAGTAGATGGTCAAATGGTGTGCTTTAC  
F S P V D \*

X  
h  
o  
i

481 ATATAAAAATAAAAGTGTGATGTAAAAAAAAAAAAAAAAAAACTCG  
polyadenylation signal poly (A) tail (26)

537 AGAGTATTCTAGAGCGGCCGCGGGCCCATCGTTTCCACCC

FIG 2.6a



**FIG 2.6b**

A. Mature Tm 13.17 amino acid residue

1 LTEAQIEKLN KISKKCQNES GVSQEIIITKA RNGDWEDDPK LKRQVFCVAR  
51 NAGLATESGE VVVDVLREKV RKVTDNDEET EKIINKCAVK RDTVEETVFN  
101 TFKCVMKNKP KFSPVD

B. Summary of the composition analysis for the mature Tm 13.17 sequence:

<u>Residue</u>	<u>Number</u>	<u>Mole Percent</u>
A = Ala	6	5.172
B = Asx	0	0.000
C = Cys	4	3.448
D = Asp	8	6.897
E = Glu	13	11.207
F = Phe	4	3.448
G = Gly	4	3.448
H = His	0	0.000
I = Ile	6	5.172
K = Lys	16	13.793
L = Leu	5	4.310
M = Met	1	0.862
N = Asn	8	6.897
P = Pro	3	2.586
Q = Gln	4	3.448
R = Arg	6	5.172
S = Ser	5	4.310
T = Thr	8	6.897
V = Val	14	12.069
W = Trp	1	0.862
Y = Tyr	0	0.000
Z = Glx	0	0.000

Molecular weight = 13171.96; Residues = 116; Average Residue Weight = 113.551

Charge = 1; Isoelectric point = 7.74.

FIG 2.6c

ପ୍ରକାଶକ ପତ୍ର

1	AGTGGATCCAAAGGATT CGGCACGAGACTACTAAGATGRA	Tm 13.17 B 1
41	OTTOCTCTOTTOCTCTAACTCTCCCTCATTCCTGTTGOTCACACA	Tm 13.17
1	CTTACTTCTCTCATTCCTGTTGOTCACACA	B 1
81	↓	
28	GTTCAGGCCCTGACCGAGGCAACAAATTGAGAAACTGAAACRA	Tm 13.17
	GTTCAGGCCATTAACCTAGGAGGACCTTGAGCTACTGAGCCCA	B 1
121	AATTCAGCAAATTAATGTTCAAAATGAAAGTGGAGTGTGCGCRA	Tm 13.17
68	AAAACCACGGCAAGAGTGCAAGAACCTGAAAGTGGAGTGTGCGCRA	B 1
161	AGAGATCATARACCAAGCTCGCRAAGCTGAGGACCGGAGGAC	Tm 13.17
118	AGACGTCATAARGAGAGCTCGCRAAGCTGAGGACCGGAGGAC	B 1
201	ATCCCTAAACTGAAACCGCCARAGTTTTCGCGTGGCCAGGAGA	Tm 13.17
148	ACCCCCAAACTGAAATOCACACTTCTTCGCGTGGCCAGGAGA	B 1
241	ACGCCCGGCTGGCCACGGARATCGGGAGAGGGTGCTGGTCGGA	Tm 13.17
188	CACTCGAATAGTGCGCGGARATCGGGAGAGGGTGCTGGTCGGA	B 1
281	CCTGTTGAGGGAGAGGTTGAGGAGTGTGAGGAGGTGCTGGTCGGA	Tm 13.17
228	CACGTTCAAGGAGAGGTTGAGGAGTGTGACGAGTGTGACGATGAT	B 1
321	GAAGAAACTCTGAGAAATCATCAGAAATAGTGGCGGCGCGTCAAGA	Tm 13.17
268	GAAGAAAGGCGAGAGATGTTGAGGAGTGTGACGAGTGTGACGATCTG	B 1
361	GAGATACTGTTGAGAGGAGCTGTTCAATACCTTCAATG	Tm 13.17
308	AACACACACTCCGGAGATAACGCCATTGAGTTACACCAATG	B 1
401	TGTCATGAAARACAGAGCCAAAGGTTCTCACCGAGTTGATTGAA	Tm 13.17
348	TGTRATTGAGGACAGGCCCAGTTCT	B 1
441	ACCAACACGAGACTAGTAGATGTTGAGTGTGTTCAATG	Tm 13.17
388	OAC TATTGCTGAGAA	B 1
481	ATATRAAATGTTCTGRTGTA	Tm 13.17
428	GCACAA	B 1

FIG 2.7

Tm 13.17	3	EAQIEKLNKISKKCQNESGVSQEIITKARNGDWEDDPKLKRQVFCVARNA 52
		..    ..  .  ..    :  :..    :       :   : ..
AFP-3	1	ETPREKLQHSDACKAESGVSEESLNKVRNREEVDDPKLKEHAFCILKRA 50
Tm 13.17	53	GLATESGEVVVDVLREKVRKVTDNDEETEKIINKCAVKRDTVEETVFNTF 102
		: ..   . :  ::. .. .::. ...:::       :    .. . :
AFP-3	51	GFIDASGEFQLDHIKTKFKENSEHPEKVDDLVAKCAVKKDTPQHSSADFF 100
Tm 13.17	103	KCVMKNKP 110
		. :
AFP-3	101	KCVHDNRS 108

Percent identity: 39.8 (identical amino acids; Percent similarity: 58.3 (identical amino acids plus conservative amino acids).

**FIG 2.8**

09829298 - 0000204

Tm 13.17

AFP-3

B Protein

M	K	L	L	C	C	L	I	S	L	I	L	L	V	T	V	Q	A
M	K	L	L	L	C	L	V	L	V	A	L	V	A	A	T	Y	A
L	T	S	L	I	L	I	L	L	V	A	V	Q	A				

FIG 2.9

093200Z SEP 80

Tm 13.17    NH<sub>2</sub>-L T E A Q I E K L N K I S K K C Q N E  
Tm 12.86    NH<sub>2</sub>-L T D E Q I Q K R N K I S K E ? Q Q V

FIG 2.10

06022960 06022960

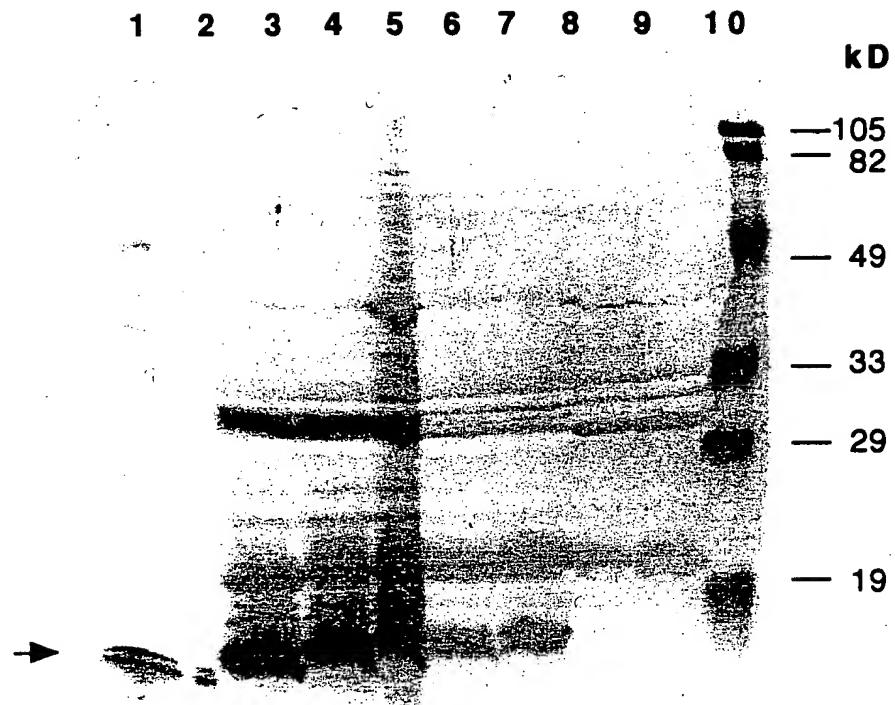


FIG 2.11

Tm13.17 B1 AFP-3

Tm 12.86	1	L T D E Q I Q K R N K I S K E ? Q Q V		
Tm 13.17	1	L T E A Q I E K L N K I S K K C Q N E S G V S Q E I I T K A	30	
B1	13	I T E E D L E L L R Q T S A E C K T E S G V S E D V I K R A	43	
AFP-3	1	E T P R E K L K Q H S D A C K A E S G V S E E S L N K V	28	
Tm13.17	31	R N G D W E D D P K L K R Q V F C V A R N A G L A T E S G E	60	
B1	44	R K G D L E D D P K L K M Q L L C I F K A L E I V A E S G E	74	
AFP-3	29	R N R E E V D D P K L K E H A F C I L K R A G F I D A S G E	58	
Tm13.17	61	V V V D V L R E K V R K V T D N D E E T E K I I N K C A V K	90	
B1	75	I E A D T F K E K L T R V T N D D E E S E K I V E K C T V T	105	
AFP-3	59	F Q L D H I K T K F K E N S E H P E K V D D L V A K C A V K	88	
Tm13.17	91	R D T V E E T V F N T F K C V M K N K P K F S P V D	116	
B1	106	E D T P E D T A F E V T K C V L K D K P N F F G D L F V	124	
AFP-3	89	K D T P Q H S S A D F F K C V H D N R S	108	

FIG 2.12

1 GGCACGAGCAAAAATGAAACTCCTCTTGTGCTTGCCTCGCCGCC  
 M K L L C F A F A A  
 47 ATCGTCATCGGAGCTCAGGCTCTCACCGACGAACAGATAACAGAAA  
 I V I G A Q A L T D E Q I Q K ↑  
 92 AGGAACAAAGATCAGCAAAGAACGCCAGCAGGTGTCCGGAGTGTCC  
 R N K I S K E C Q Q V S G V S  
 137 CAAGAGACGATCGACAAAGTCCGCACAGGTGTCTTGGTCGATGAT  
 Q E T I D K V R T G V L V D D  
 182 CCCAAAATGAAGAACGACGTCCCTCTGCTTCTCGAAGAAAAACTGGA  
 P K M K H V L C F S K K T G  
 226 GTGGCAACCGAACGCCGGAGACACCAATGTGGAGGTACTCAAAGCC  
 V A T E A G D T N V E V L K A  
 271 AAGCTGAAGCATGTGGCCAGCGACGAAGAGGGTGGACAAGATCGTG  
 K L K H V A S D E E V D K I V  
 316 CAGAAGTGCCTGGTCAAGAACGCCACACCAAGAGGGAAACGGCTTAT  
 Q K C V V K K A T P E E T A Y  
 361 GACACCTTCAAGTGTATTACGACAGCAAACCTGATTCTCTCCT  
 D T F K C I Y D S K P D F S P  
 406 ATTGATTAATTGTTTGATTTGACTGAATTGACAATAAAGGT  
 I D \* polyadenylation signal  
 451 ACTATCGTTATGTAAAAAAAAAAAAAA

poly (A) tail

**FIG 3.0**

Sequence Data

```

1   GGCACGGAGCAAAAATGAAACTCCTCTTGTGCTTGCTTCGCCGCC
      M   K   L   L   L   C   F   A   F   A   A
      |   |   |   |   |   |   |   |   |   |
      I   V   I   G   A   Q   A   L   T   D   E   Q   I   Q   K
      |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
      R   N   K   I   S   K   E   C   Q   Q   V   S   G   V   S
      |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
      Q   E   T   I   D   K   V   R   T   G   V   L   V   D   D
      |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
      CCCAAAATGAAGAACGACGTCCCTCTGCTTCTCGAAGAAAATGGAA
      P   K   M   K   K   H   V   L   C   F   S   K   K   T   G
      |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
      GTGGCAACCGAAGCCGGAGACACCAATGTGGAGGTACTCAAAGCC
      V   A   T   E   A   G   D   T   N   V   E   V   L   K   A
      |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
      AAGCTGAAGCATGTGGCCAGCGACGAAGAAGTGGACAAGATCGTG
      K   L   K   H   V   A   S   D   E   E   V   D   K   I   V
      |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
      CAGAACGTGCGTGGTCAAGAACGGCACACCAAGAGGAACGGCTTAT
      Q   K   C   V   V   K   K   A   T   P   E   E   T   A   Y
      |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
      GACACCTTCAAGTGTATTTACGACAGTAACCTGATTTCTCTCCT
      D   T   F   K   C   I   Y   D   S   K   P   D   F   S   P
      |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
      ATTGATTAATTGTTTGTATTTGACTGAATTTGACAAATAAGGT
      I   D   *   |   |   |   |   |   |   |   |   |   |   |   |
      ACTATCGTTATGAAAAAAAAAAAAAAA
      |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
      polyadenylation signal
      |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
      poly (A) tail
      |   |   |   |   |   |   |   |   |   |   |   |   |   |   |

```

FIG 3.1

卷之三

start

FIG 3.2

Predicted Amino Acid

Composition of 2-2 and 2-3

Analysis	Whole Protein
Molecular Weight	12843.80 m.w.
Length	115
1 microgram =	77.859 pMoles
Molar Extinction coefficient	3040±5%
1 A(280) =	4.22 mg/ml
Isoelectric Point	7.11
Charge at pH 7	0.13

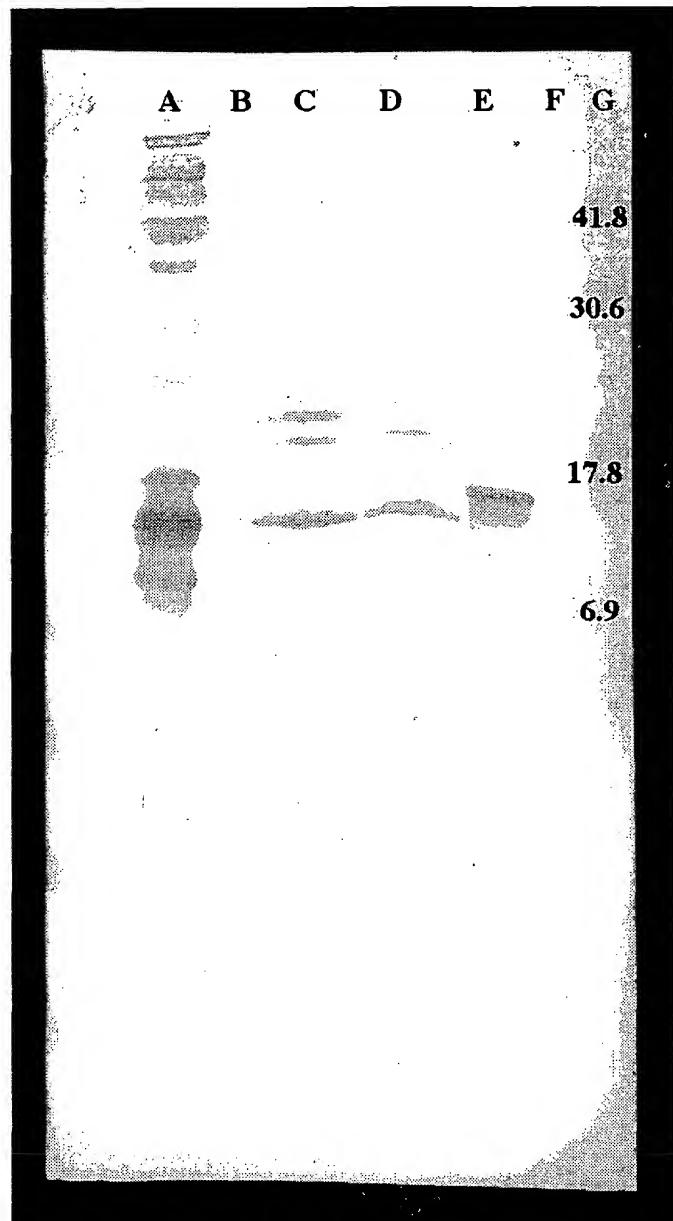
Whole Protein Composition Analysis

Amino Acid(s)	Number count	% by weight	% by frequency
Charged (RKHYCDE)	48	47.19	41.74
Acidic (DE)	20	18.90	17.39
Basic (KR)	20	20.40	17.39
Polar (NCQSTY)	30	25.35	26.09
Hydrophobic (AILFWV)	34	27.26	29.57
A Ala	6	3.32	5.22
C Cys	4	3.21	3.48
D Asp	11	9.86	9.57
E Glu	9	9.05	7.83
F Phe	3	3.44	2.61
G Gly	4	1.78	3.48
H His	2	2.14	1.74
I Ile	6	5.29	5.22
K Lys	18	17.97	15.65
L Leu	5	4.41	4.35
M Met	1	1.02	0.87
N Asn	2	1.78	1.74
P Pro	4	3.02	3.48
Q Gln	6	5.98	5.22
R Arg	2	2.43	1.74
S Ser	7	4.75	6.09
T Thr	9	7.08	7.83
V Val	14	10.80	12.17
W Trp	0	0.00	0.00
Y Tyr	2	2.54	1.74
B Asx	0	0.00	0.00
Z Glx	0	0.00	0.00
X Xxx	0	0.00	0.00
Ter	0	0.00	0.00

FIG 3.3

09826296 - 060204

0.962 0.900 " 0.862



**FIG 3.4**

Lane

1 2 3 4 5

a → b →

577 bp  
483 bp

FIG 4.0

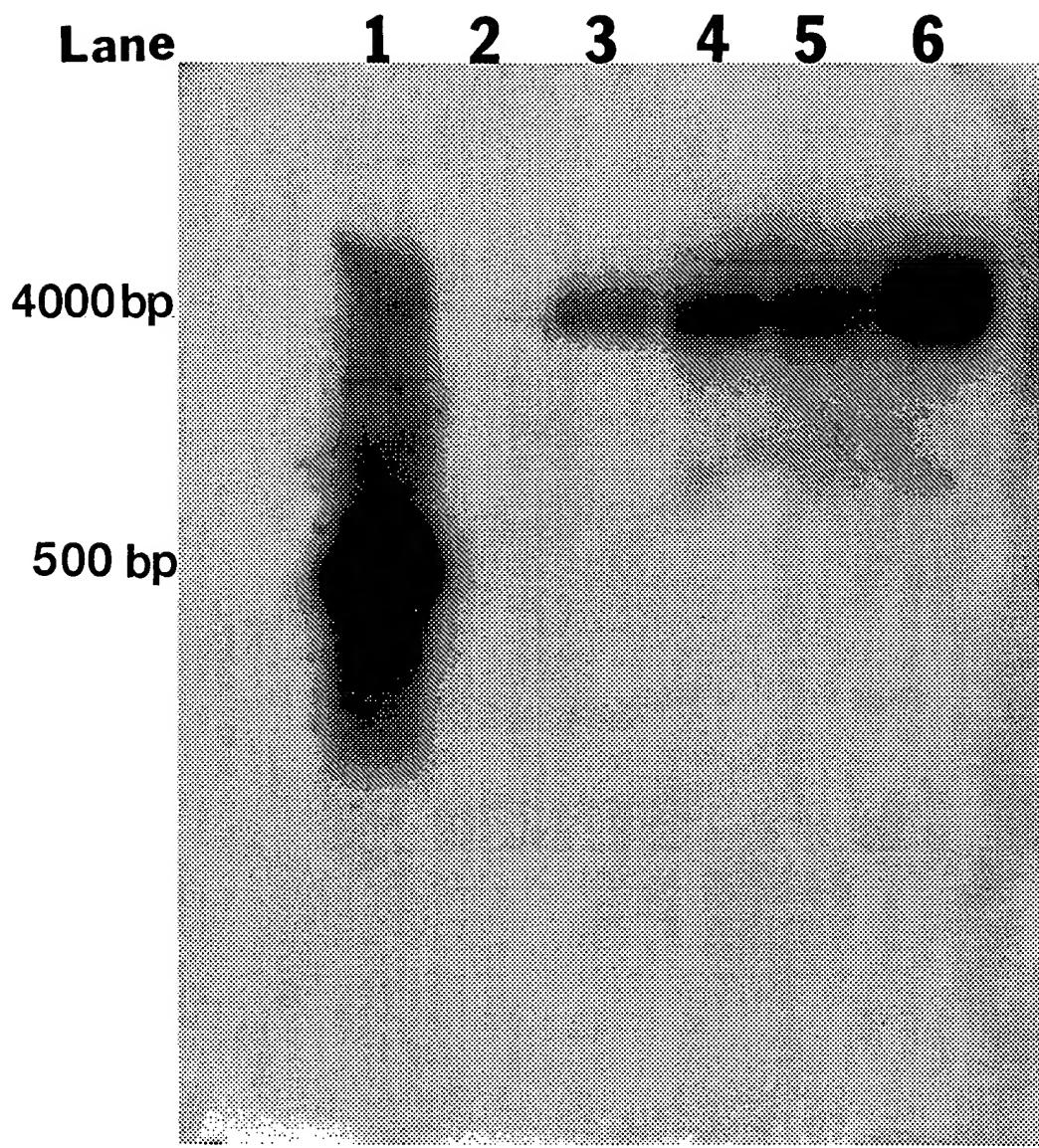


FIG 4.1

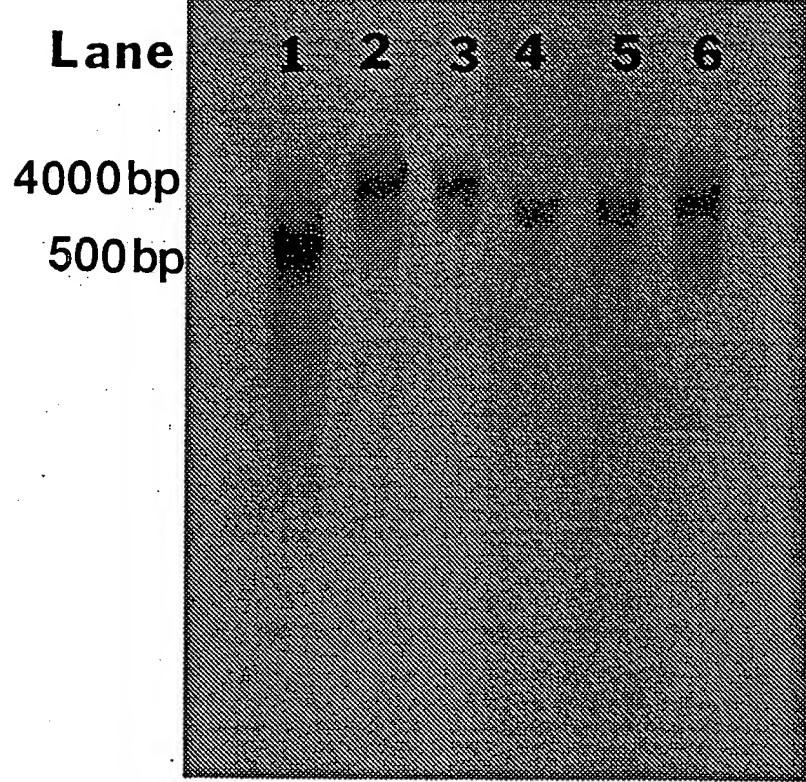


FIG. 4.2

□ □ □ □ □ □

**B.**

**A.**

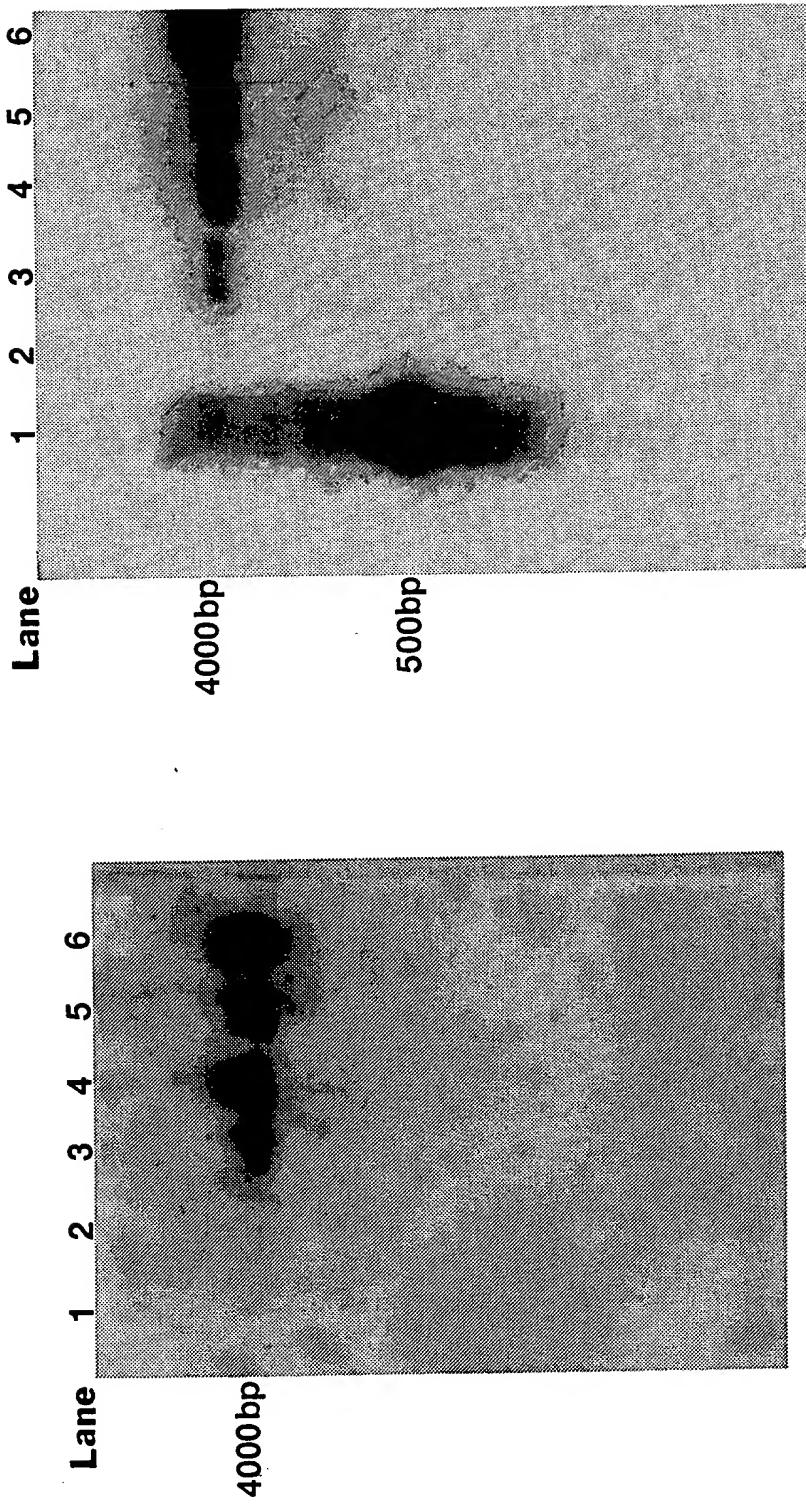


FIG. 4.3

702090 "0629950

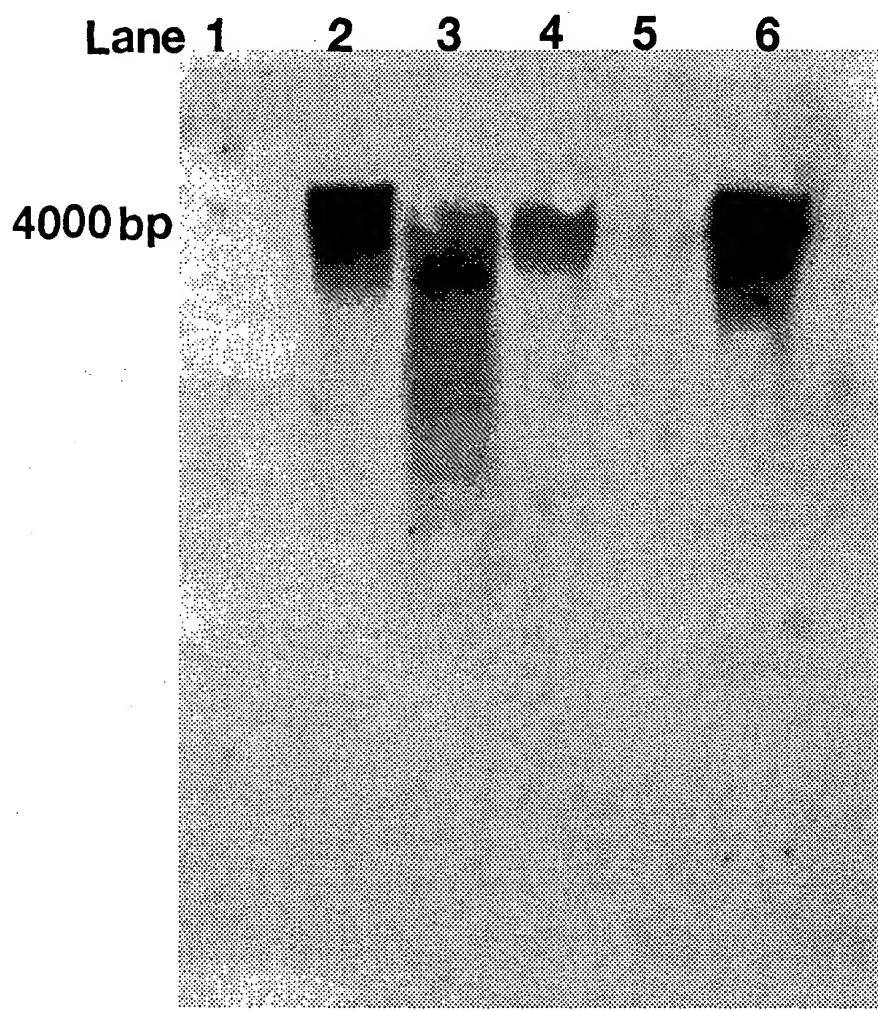
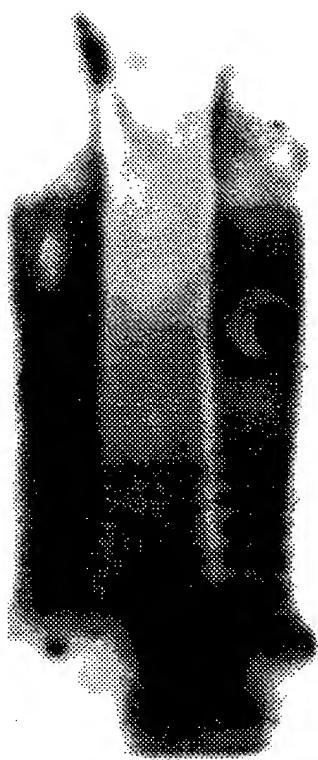


FIG 4.4

**Lane**      **1**    **2**    **3**    **4**    **5**



23130

9416

4361

2322

2027

564

**FIG 4.5**

Tm 13.17 cDNA

1 AGTGGATCCAAAGAATTGGCACGAGACTACTAAGATCAAGTTGCTCTGTTGTCTAATCT  
M K L L C C L I S

61 CCCTCATCTGTTGGTCACAGTTCAAGGCCCTGACCGAGGCACAAATTGAGAAACTGAACA  
L I L L V T V Q A L T E A Q I E K L N K  
  ↑ Forward Primer

121 AGATCAGCAAAAATGTCAAAATGAAAGTGGAGTGTGCAAGAGATCATAACCAAAGCTC  
I S K K C Q N E S G V S Q E I I T K A R

181 GCAACGGTGACTGGGAGGACGATCCTAAACTGAAACGCCAAGTTTGCGTGGCCAGGA  
N G D W E D D P R L K R Q V F C V A R N

241 ACGCCGGTCTGGCCACGGAACTGGGAGAGGTGGTGGTCGACGTGTTGAGGGAGAACGGTGA  
A G L A T E S G E V V V D V L R E K V R

301 GGAAGGTCACTGACAACGACGAAGAAACTGAGAAAATCATCAATAAGTGCGCCGTCAAGA  
K V T D N D E E T E K I I N K C A V K R  
  Reverse Primer

361 GA G A T A C T G T T G A A G A G A C G G T G T C A A T A C T T C A A A T G T G T C A T G A A A A A C A A G G C A A  
D T V E E T V F N T F K C V M K N K P K

421 AGTTCTACCAGTTGATTGAACCACGACTAGTAGATGGTTCAAATGGTGTGCTTAC  
F S P V D \*

481 ATATAAAAATAAAGT~~TTT~~CTGATGTAAAAAAAAAAAAAAACTC

FIG. 4.6 a

B.

Forward Primer

2-2           LT D E Q I Q K R N K I S K E C Q Q V S G V S Q E T I D K V R T G V L V  
Tm 13.17     L T E A Q I E K L N K I S K K C Q N E S G V S Q E I I T K A R N G D W E  
B2           L T E E D L Q L L R Q T S A E C K T E S G A S E A V I K K A R K G D L E  
AFP-3       E T P R E K L K Q H S D A C K A E S G V S E E S L N K V R N R E E V

2-2           D D P K M K K H V L C F S K K T G V A T E A G D T N V E V L K A K L K H  
Tm 13.17     D D P K L K R Q V F C V A R N A G L A T E S G E V V V D V L R E K V R K  
B2           D D P K L K M Q L L C I F K A L E I V A E S G E I E A D T F K E K L T R  
AFP-3       D D P K L K E H A F C I L K R A G F I D A S G E F Q L D H I K T K F K E

Reverse Primer

2-2           V A S D E E V D K I V Q K C V V V K K A T P E E T A Y D T F K C I Y D S  
Tm 13.17     V T D N D E E T E K I I N K C A V K R D T V E E T V F N T F K C V M K N  
B2           V T N D D E E S E K I V E K C T V T E D T P E D T A F E V T K C V L K D  
AFP-3       N S E H P E K V D D L V A K C A V K K D T P Q H S S A D F F K C V H D N

2-2           K P D F S P I D  
Tm 13.17     K P K F S P V D  
B2           K P N F F G D L F V  
AFP-3       R S

0 9 8 7 6 5 4 3 2 1 0

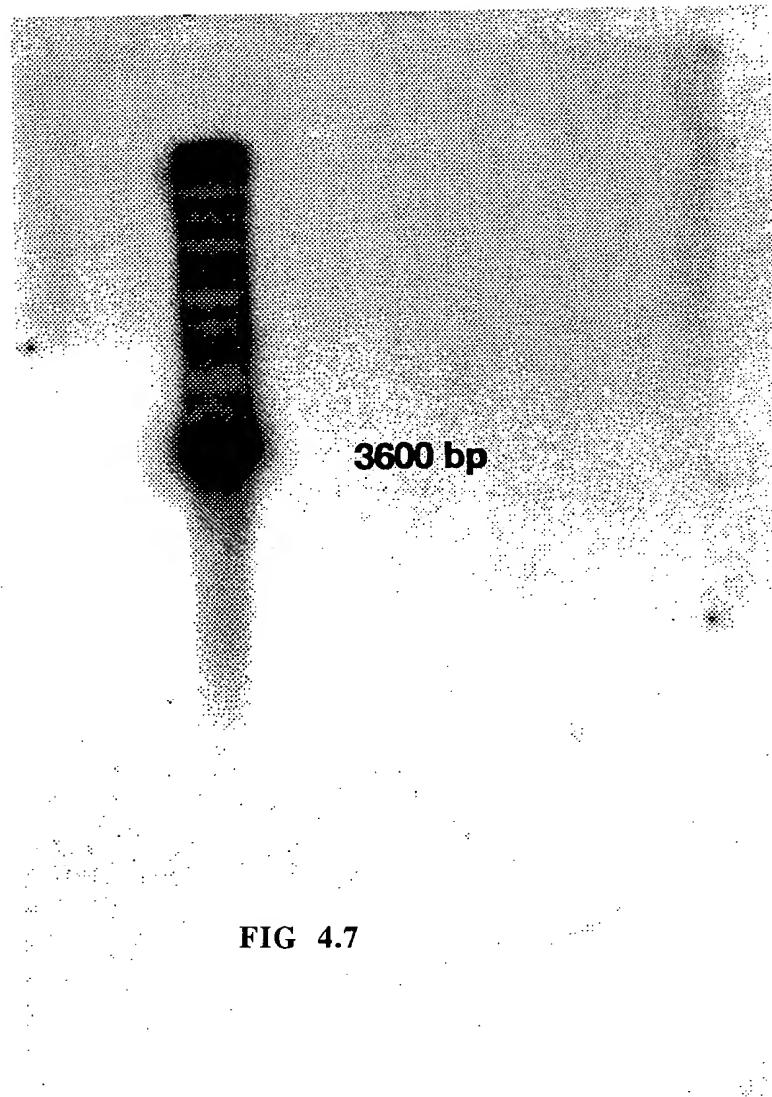
C.

percent % composition

Primer	A	C	G	T	Melting Temperature (°C)
Forward	28.6	14.3	42.9	14.3	44.0
Reverse	25.0	31.3	6.3	37.5	44.0

FIG 4.6

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**FIG. 4.7**

098765432109876543210

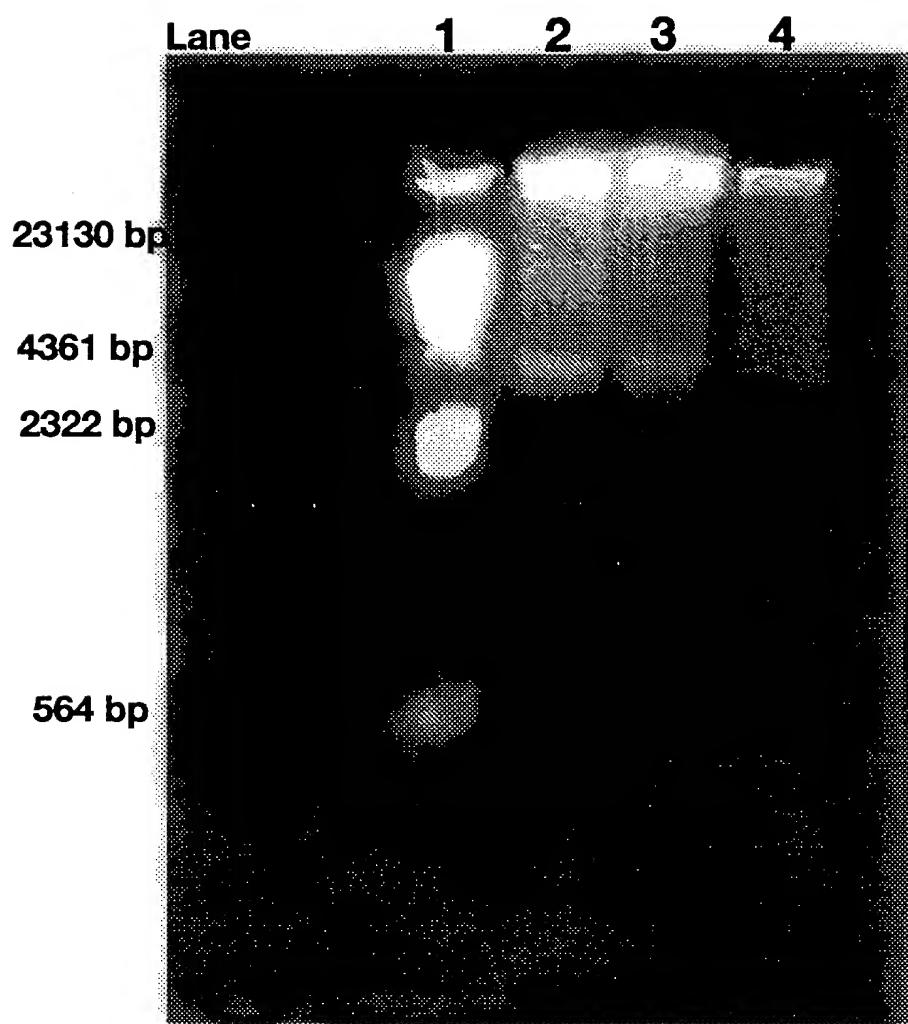


FIG 4.8

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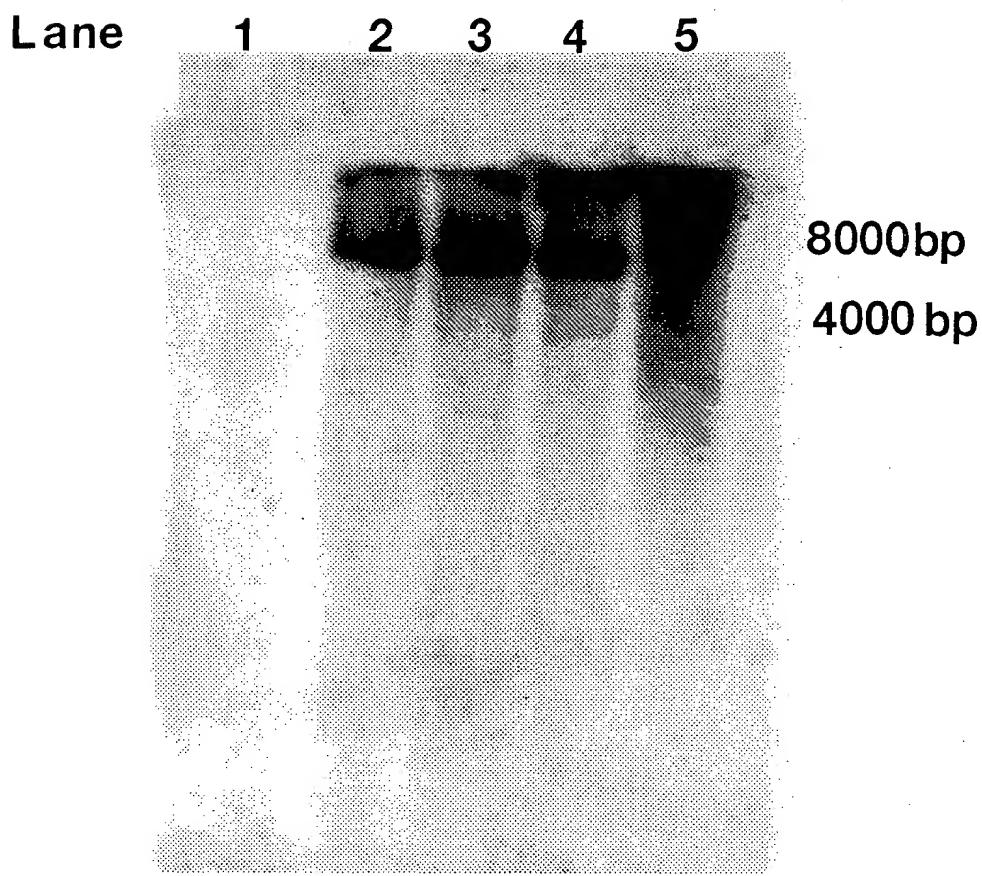


FIG 4.9

DECODED SEQUENCES

1    GGCACGGAGCAAAAATGAAACTCCTCTTGTGCTTTCGCGGCC  
       M    K    L    L    L    C    F    A    F    A    A

47    ATCGTCATCGGAGCTCAGGCTCTCACCGACGAACAGATAACAGAAA  
       I    V    I    G    A    Q    A    L    T    D    E    Q    I    Q    K

92    AGGAACAAGATCAGCAAAGAATGCCAGCAGGTGTCCGGAGTGTCC  
       R    N    K    I    S    K    E    C    Q    Q    V    S    G    V    S

137   CAAGAGACGATCGACAAAGTCCGCACAGGTGTCTGGTCGACGAT  
       Q    E    T    I    D    K    V    R    T    G    V    L    V    D    D

182   CCCAAAAATGAAGAACGACGTCCCTCTGCTTCTCGAAGAAAATGGAA  
       P    K    M    K    K    H    V    L    C    F    S    K    K    T    G

226   GTGGCAACCGAAGGCCGGAGACACCAATGTGGAGGTACTCAAAGCC  
       V    A    T    E    A    G    D    T    N    V    E    V    L    K    A

271   AAGCTGAAGCATGTGGCCAGCGACGAAGAGGTGGACAAGATCGTG  
       K    L    K    H    V    A    S    D    E    E    V    D    K    I    V

316   CAGAACGTGCGTGGTCAAGAACGGCCACACCAAGAGGAAACGGCTTAT  
       Q    K    C    V    V    K    K    A    T    P    E    E    T    A    Y

361   GACACCTTCAAGGTTATTACGACAGTAAACCTGATTTCTCTCCT  
       D    T    F    K    V    I    Y    D    S    K    P    D    F    S    P

406   ATTGATTAATTGTTTGTATTTGACTGAATTTGACAAATAAGGT  
       I    D

451   ACTATCGTTATGTAAAAAAAAAAAAAA polyadenylation signal

poly (A) tail

FIG. 4.10 a

Analysis	Whole Protein
Molecular Weight	12839.70 m.w.
Length	115
1 microgram =	77.883 pMoles
Molar Extinction coefficient	2920±5%
1 A(280) =	4.40 mg/ml
Isoelectric Point	7.14
Charge at pH 7	0.16

Predicted Amino Acid

Composition of 3-4

Whole Protein Composition Analysis

Amino Acid(s)	Number count	% by weight	% by frequency
Charged (RKHYCDE)	47	46.41	40.87
Acidic (DE)	20	18.91	17.39
Basic (KR)	20	20.41	17.39
Polar (NCQSTY)	29	24.55	25.22
Hydrophobic (AILFWV)	35	28.04	30.43
A Ala	6	3.32	5.22
C Cys	3	2.41	2.61
D Asp	11	9.86	9.57
E Glu	9	9.05	7.83
F Phe	3	3.44	2.61
G Gly	4	1.78	3.48
H His	2	2.14	1.74
I Ile	6	5.29	5.22
K Lys	18	17.97	15.65
L Leu	5	4.41	4.35
M Met	1	1.02	0.87
N Asn	2	1.78	1.74
P Pro	4	3.02	3.48
Q Gln	6	5.99	5.22
R Arg	2	2.43	1.74
S Ser	7	4.75	6.09
T Thr	9	7.09	7.83
V Val	15	11.58	13.04
W Trp	0	0.00	0.00
Y Tyr	2	2.54	1.74
B Asx	0	0.00	0.00
Z Glx	0	0.00	0.00
X Xxx	0	0.00	0.00
Ter	0	0.00	0.00

FIG. 4.10 b

1 GGCACGAGCAAAAATGA  
M K L L L C F A F A A

47 ATCGTCATCGGAGCTCAGGCTCTCACCGATGAACAGATAACAGAAA  
I V I G A Q A **L** T D E Q I Q K

92 AGGAACAAGATCAGCAAAGAATGCCAGCAGGAGTCCGGAGTGTCC  
R N K I S K E C Q Q E S G V S

137 CAAGAGACGATCGACAAAGTCCGCACAGGTGTCTTGGTCGACGAT  
Q E T I D K V R T G V L V D D

182 CCCAAAATGAAGAACGACCGTCCCTCTGCCTCTCGAACAGAGAACTGGA  
P K M K K H V L C F S K R T G

226 GTGGCAACCGAACGCCAGACACCAATGTGGAGGTACTCAAAGCC  
V A T E A G D T N V E V L K A

271 AAGCTGAAGCATGTGGCCAGCGACGAAGAACGTGGACAAAGATCGTG  
K L K H V A S D E E V D K I V

316 CAGAACGTGCGTGGTCAAGAACGCCACACCAAGAGGAACGGCTTAT  
Q K C V V K K A T P E E T A Y

361 GACACCTTCAAGTGTATTACGACAGTAACCTGATTTCTCTCCT  
D T F K V I Y D S K P D F S P

406 ATTGATTAATTGTTTGTATTTGACTGAATTGACAAATAAGGT  
I D polyadenylation signal

451 ACTATCGTTATGAAAAA  
 poly (A) tail

FIG. 4.11 a

## Predicted Amino Acid

## Composition of 3-9

Analysis	Whole Protein
Molecular Weight	12871.80 m.w.
Length	115
1 microgram =	77.689 pMoles
Molar Extinction coefficient	3040±5%
1 A(280) =	4.23 mg/ml
Isoelectric Point	7.11
Charge at pH 7	0.13

## Whole Protein Composition Analysis

Amino Acid(s)	Number count	% by weight	% by frequency
Charged (RKHYCDE)	48	47.31	41.74
Acidic (DE)	20	18.86	17.39
Basic (KR)	20	20.57	17.39
Polar (NCQSTY)	30	25.29	26.09
Hydrophobic (AILFWV)	34	27.20	29.57
A Ala	6	3.31	5.22
C Cys	4	3.21	3.48
D Asp	11	9.84	9.57
E Glu	9	9.03	7.83
F Phe	3	3.43	2.61
G Gly	4	1.77	3.48
H His	2	2.13	1.74
I Ile	6	5.28	5.22
K Lys	17	16.93	14.78
L Leu	5	4.40	4.35
M Met	1	1.02	0.87
N Asn	2	1.77	1.74
P Pro	4	3.02	3.48
Q Gln	6	5.97	5.22
R Arg	3	3.64	2.61
S Ser	7	4.74	6.09
T Thr	9	7.07	7.83
V Val	14	10.78	12.17
W Trp	0	0.00	0.00
Y Tyr	2	2.54	1.74
B Asx	0	0.00	0.00
Z Glx	0	0.00	0.00
X Xxx	0	0.00	0.00
Ter	0	0.00	0.00

FIG. 4.11 b

TOEYZEGE " DEPOZD

1 GGCACGAGCAAAATGAAACTCCTCTTGTGCTTGCCTCGCCGCC  
 M K L L L C F A F A A

47 ATCGTCATCGGAGCTCAGGCTCTCACCGACGAACAGATAACAGAAA  
 I V I G A Q A L T D E Q I Q K ↑

92 AGGAACAAGATCAGCAAAGAGTGCAGCAGGTGTCCGGAGTGTCC  
 R N K I S K E C Q Q E S G V S

137 CAAGAGACGATCGACAAAGTCCGCACAGGTGTCTTGGTCGACGAT  
 Q E T I D K V R T G V L V D D

182 CCCAAAATGAAGAAGCACGTCCTCTGCTTCTCGAAGAAAACGGAA  
 P K M K K H V L C F S K R T G

226 GTGGCAACCGAAGGCCGGAGACACCAATGTGGAGGTACTCAAAGCC  
 V A T E A G D T N V E V L K A

271 AAGCTGAAGCATGTGGCCAGCGACGAAGAACGTTGGACAAAGATCGTG  
 K L K H V A S D E E V D K I V

316 CAGAAGTGCCTGGTCAAGAACGGCCACACCAAGAGGAAACGGCTTAT  
 Q K C V V K A T P E E T A Y

361 GACACCTTCAAGTGTATTTACGACAGTAAACCTGATTTCTCTCCT  
 D T F K V I Y D S K P D F S P

406 ATTGATTAAATTGTTTGTATTTGGCTGAATTTGACAAAGGT  
 I D

polyadenylation signal

FIG. 4.12 a

**Predicted Amino Acid****Composition of 7-5**

<b>Analysis</b>	<b>Whole Protein</b>
Molecular Weight	12843.80 m.w.
Length	115
1 microgram =	77.859 pMoles
Molar Extinction coefficient	3040±5%
1 A(280) =	4.22 mg/ml
Isoelectric Point	7.11
Charge at pH 7	0.13

**Whole Protein Composition Analysis**

<b>Amino Acid(s)</b>	<b>Number count</b>	<b>% by weight</b>	<b>% by frequency</b>
Charged (RKHYCDE)	48	47.19	41.74
Acidic (DE)	20	18.90	17.39
Basic (KR)	20	20.40	17.39
Polar (NCQSTY)	30	25.35	26.09
Hydrophobic (AILFWV)	34	27.26	29.57
A Ala	6	3.32	5.22
C Cys	4	3.21	3.48
D Asp	11	9.86	9.57
E Glu	9	9.05	7.83
F Phe	3	3.44	2.61
G Gly	4	1.78	3.48
H His	2	2.14	1.74
I Ile	6	5.29	5.22
K Lys	18	17.97	15.65
L Leu	5	4.41	4.35
M Met	1	1.02	0.87
N Asn	2	1.78	1.74
P Pro	4	3.02	3.48
Q Gln	6	5.98	5.22
R Arg	2	2.43	1.74
S Ser	7	4.75	6.09
T Thr	9	7.08	7.83
V Val	14	10.80	12.17
W Trp	0	0.00	0.00
Y Tyr	2	2.54	1.74
B Asx	0	0.00	0.00
Z Glx	0	0.00	0.00
X Xxx	0	0.00	0.00
Ter	0	0.00	0.00

PREDICTED AMINO ACID COMPOSITION

**FIG. 4.12 b**

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FIG. 4.13

T D C D G C A C E G

↓

2-2	M	K	L	L	C	F	A	F	A		V	!	G	A	Q	A	L	T	D	E	Q	!
2-3	M	K	L	L	C	F	A	F	A		V	!	G	A	Q	A	L	T	D	E	Q	!
3-4	M	K	L	L	C	F	A	F	A		V	!	G	A	Q	A	L	T	D	E	Q	!
3-9	M	K	L	L	C	F	A	F	A		V	!	G	A	Q	A	L	T	D	E	Q	!
7-5	M	K	L	L	C	F	A	F	A		V	!	G	A	Q	A	L	T	D	E	Q	!

2-2 DDPKMKHHVLCFKSKKTGVATEAGDTNVEVLKAKLKKHVASDDEEVDKIVQKCVVK  
 2-3 DDPKMKHHVLCFKSKKTGVATEAGDTNVEVLKAKLKKHVASDDEEVDKIVQKCVVK  
 3-4 DDPKMKHHVLCFKSKKTGVATEAGDTNVEVLKAKLKKHVASDDEEVDKIVQKCVVK  
 3-9 DDPKMKHHVLCFKSKKTGVATEAGDTNVEVLKAKLKKHVASDDEEVDKIVQKCVVK  
 7-5 DDPKMKHHVLCFKSKKTGVATEAGDTNVEVLKAKLKKHVASDDEEVDKIVQKCVVK

2-2 ATPEETAYDTFKC|YDSSKPDFSPID\*  
 2-3 ATPEETAYDTFKC|YDSSKPDFSPID\*  
 3-4 ATPEETAYDTFKC|YDSSKPDFSPID\*  
 3-9 ATPEETAYDTFKC|YDSSKPDFSPID\*  
 7-5 ATPEETAYDTFKC|YDSSKPDFSPID\*

FIG. 4.14

(kDa)	(% mole)													% most hydrophilic							
MW	AA	Cys	Pro	Phe	Ile	Val	Met	Leu	% most hydrophobic	Gly	Ala	Tyr	His	Trp	Asx	Glx	Arg	Lys	Ser	Thr	
Tm	12.86	117	3.2	3.0	3.4	4.4	8.5	2.0	4.4	28.9	3.1	3.9	3.8	3.2	ND	10.7	15.0	3.6	14.9	6.8	6.3
<b>12.86</b>																					57.3
Tm	13.17	116	3.13	2.21	4.47	5.16	10.5	1.0	4.3	29.11	1.73	3.24	0	0	1.4	0	0	7.12	15.6	3.31	6.14
<b>13.17</b>																1					32.14
2.2	12.84	115	3.21	3.02	3.44	5.29	10.8	1.02	4.41	27.26	1.78	3.32	2.54	2.14	0	0	0	2.43	18.0	4.75	7.08
<b>2.2</b>																					32.23
2.3	12.84	115	3.21	3.02	3.44	5.29	10.8	1.02	4.41	27.26	1.78	3.32	2.54	2.14	0	0	0	2.43	18.0	4.75	7.08
<b>2.3</b>																					32.23
3.4	12.84	115	2.41	3.02	3.44	5.29	11.6	1.02	4.41	28.04	1.78	3.32	2.54	2.14	0	0	0	2.43	18.0	4.75	7.09
<b>3.4</b>																					32.24
3.9	12.87	115	3.21	3.02	3.43	5.28	10.8	1.02	4.40	27.20	1.77	3.31	2.54	2.13	0	0	0	3.64	16.9	4.74	7.07
<b>3.9</b>																					32.38
7.5	12.84	115	3.21	3.02	3.44	5.29	10.8	1.02	4.41	27.26	1.78	3.32	2.54	2.14	0	0	0	2.43	18.0	4.75	7.08
<b>7.5</b>																					32.23

FIG. 4.15

၁၀၅

Tm 12.86  
2-2  
2-3  
3-4  
3-9  
7-5  
Tm 13.17  
**B1**  
**B2**  
**AFP-3**

V >> V V WE E E  
V >> V V DWE E E  
G G G G D D D D  
T T T T N K K K  
D D D D T K K K  
V >> V V A A A  
D D D D K K K  
I I I I V A V V  
E E E E D E A V  
Q Q Q Q E E E E  
S S S S D D D D  
V >> V V A A V  
V >> V V A A V  
Q Q Q Q A A A A  
C C C C C C C C  
K E ? C C C C C C  
S K E E E E E E E  
R N K R R R R R R  
D E O I O O O O O O  
D E O I O O O O O O  
D E O I O O O O O O  
D E O I O O O O O O  
T T T T T T T T T T  
L L L L L L L L L L  
G A G A G A G A G  
V V V V V V V V V  
I V V V V V V V V  
A A A A A A A A A  
F F F F F F F F F  
C C C C C C C C C  
L C F A F A A A A  
L C F A F A A A A  
L C F A F A A A A  
C C L I S L I L L  
L T S L I L L L L  
L C L V L V L V L  
V A T Y V A T Y V  
V A T Y V A T Y V  
V A T Y V A T Y V

2-2  
2-3  
3-4  
3-9  
7-5  
Tm 13.17  
B1  
B2  
**AED-3**

2-2  
2-3  
3-4  
3-9  
7-5  
Tm 13.17  
**B1**  
**B2**  
**AFP-3**

FIG. 4.16

TOE090 "S6c9" 860

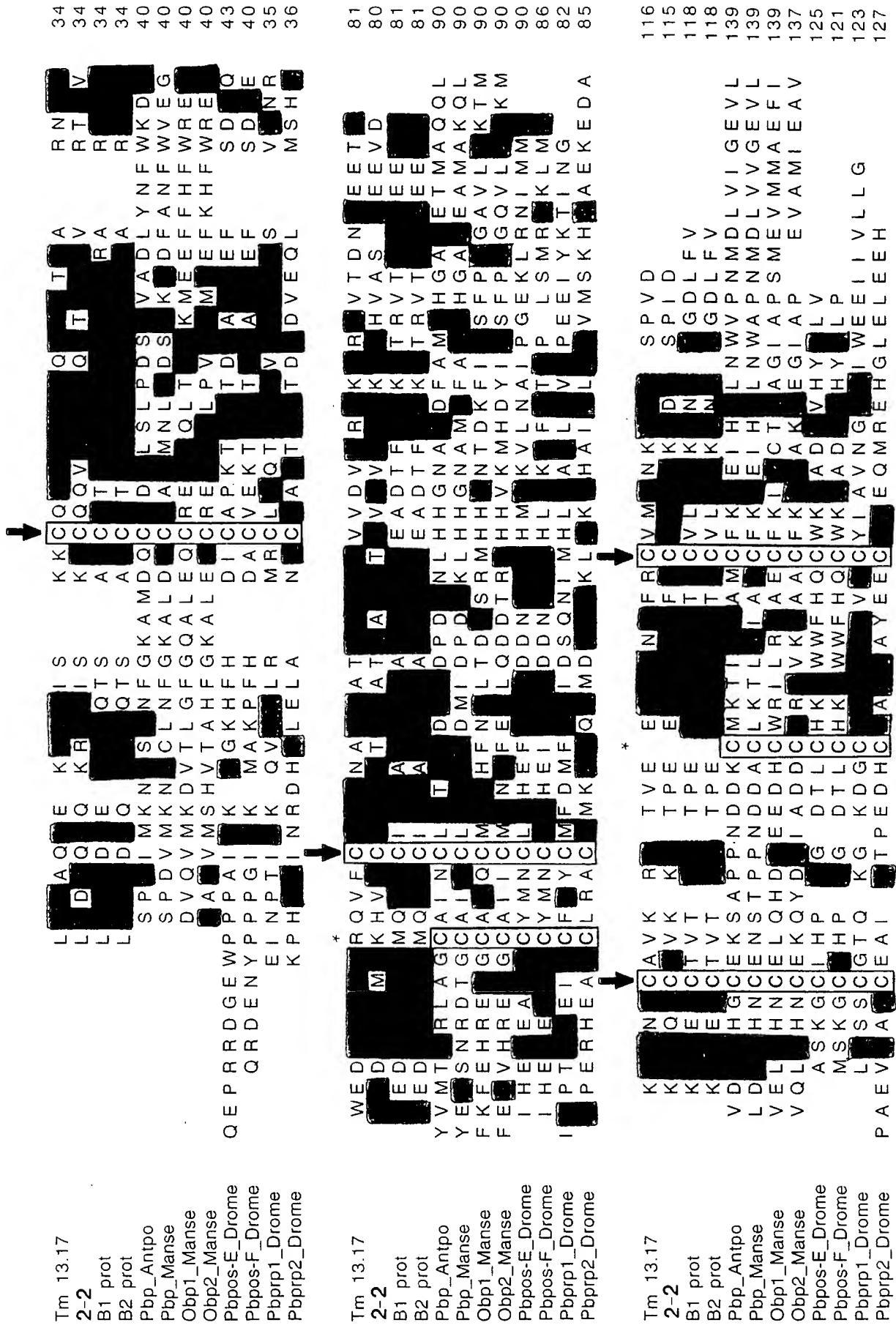


FIG. 4.17

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T<sub>m</sub> 12.86

2-2  
2-3  
3-4  
3-9  
7-5  
Tm 13.17  
**B1**  
**B2**  
**AEP-3**

**AEB-3**

FIG. 4.18

# NUCLEOTIDE SEQUENCES

PERCENT SIMILARITY

	1 <sup>2-2</sup>	2 <sup>2-3</sup>	3 <sup>3-4</sup>	4 <sup>3-9</sup>	5 <sup>7-5</sup>	6 Tm 13.17	7 B1	8 AFP-3	9 YL-1	10 DAFP-1A
1	99.1	97.3	98.4	98.2	50.4	42	42.4	20.7	20.9	1 2-2
2	0.9	99	99	99	51.5	43.2	42.7	20.2	21.3	2 2-3
3	1.6	60	98	98	50.3	42	42.1	20	20	3 3-4
4	1.6	20	80	98.4	51.3	43.7	43.6	20.4	22	4 3-9
5	1.8	25	75	45	50.4	42.5	42.9	22.2	23.1	5 7-5
6	36.9	36.4	37.2	36.4	37.1	57.2	37.4	23.3	21	6 Tm 13.17
7	39.9	41.2	41.7	40.7	41.2	30.2	39.3	21.9	22.1	7 B1
8	41.8	42.4	43.1	42.3	42.3	45.3	49.4	21.8	23.1	8 AFP-3
9	48.7	58.6	52	51.2	51.9	61.7	62.2	58.2	45.6	9 YL-1
10	51.4	62.7	46.4	46.5	46.5	60	58.1	61.8	35.5	10 DAFP-1A

PERCENT DIVERGENCE

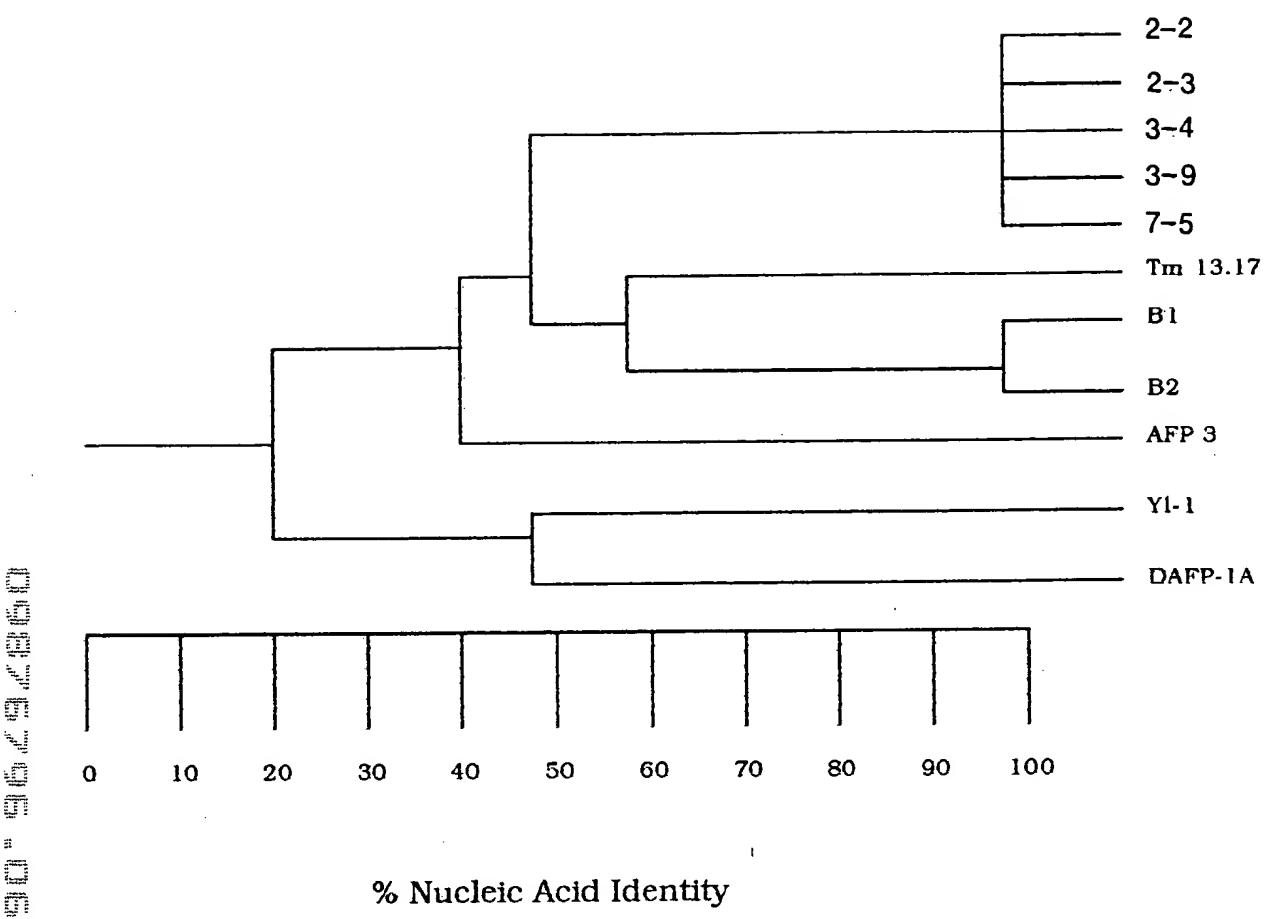
# AMINO ACID SEQUENCES

PERCENT SIMILARITY

	1 <sup>2-2</sup>	2 <sup>2-3</sup>	3 <sup>3-4</sup>	4 <sup>3-9</sup>	5 <sup>7-5</sup>	6 Tm 13.17	7 B1	8 AFP-3	9 YL-1	10 DAFP-1A
1	100	99.1	99.1	100	51.3	37.4	35.2	11.6	12	1 2-2
2	0	99.1	99.1	100	51.3	37.4	35.2	11.6	12	2 2-3
3	0.9	0.9	98.3	99.1	50.4	36.5	34.3	11.6	12	3 3-4
4	0.9	0.9	1.7	99.1	51.3	37.4	36.1	10.7	12	4 3-9
5	0	0	0.9	0.09	51.3	37.4	35.2	11.6	12	5 7-5
6	46.1	46.1	47	46.1	46.1	47.4	39.8	13.4	13.9	6 Tm 13.17
7	59.1	59.1	60	59.1	59.1	51.7	37	11.6	11.1	7 B1
8	61.7	61.7	62.6	60.7	61.7	60.2	63	10.2	8.3	8 AFP-3
9	86.7	86.7	85.7	85.7	85.7	86.8	84.2	87.5	55.6	9 YL-1
10	88.3	88.3	86.4	84.5	85.4	89.1	82.7	90.5	40.2	10 DAFP-1A

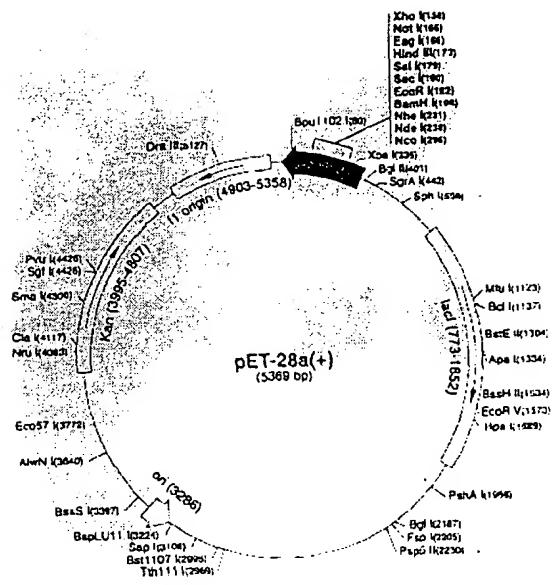
PERCENT DIVERGENCE

FIG 4.19



**FIG 4.20**

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**FIG. 5.0**

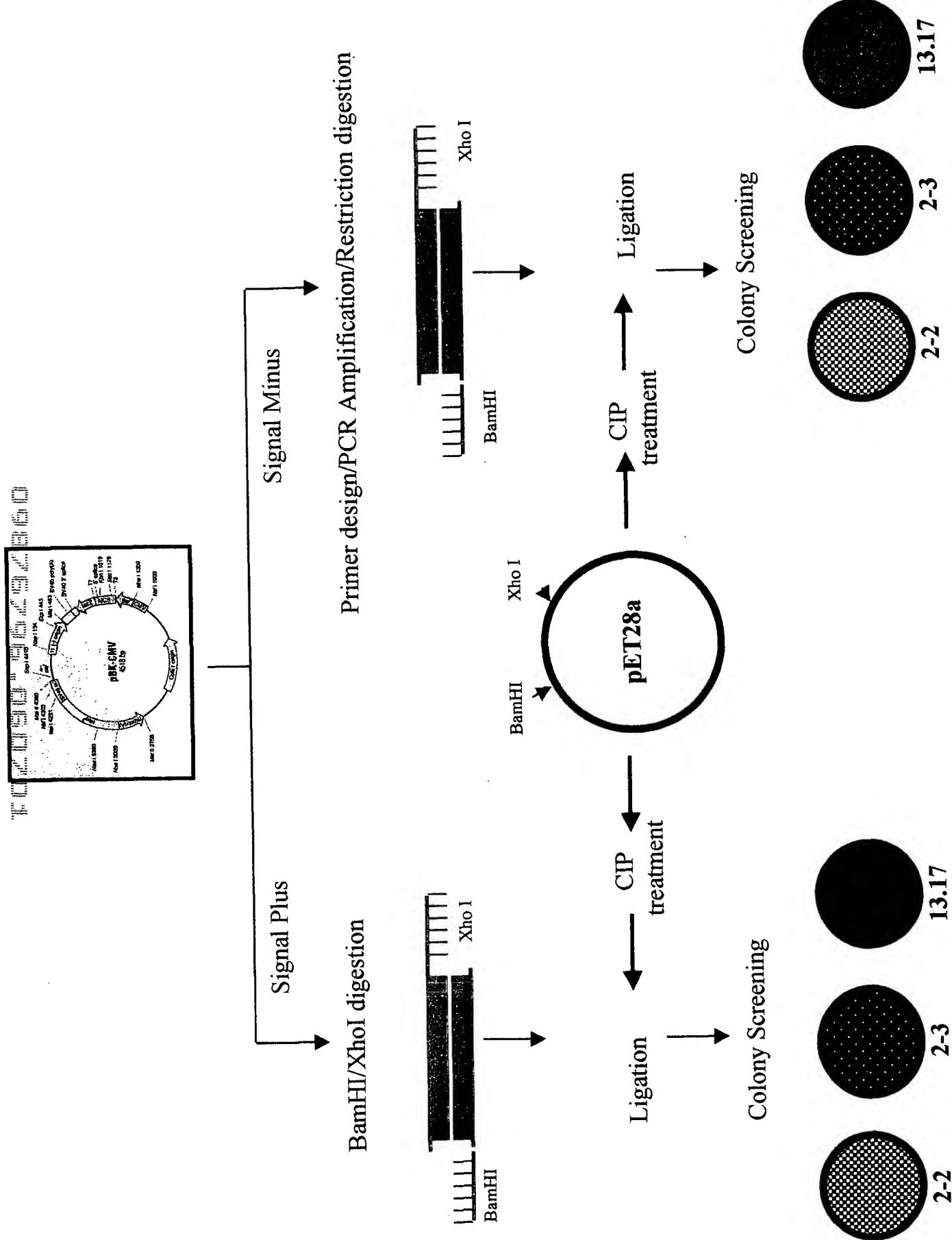


FIG. 5.1

500 bp

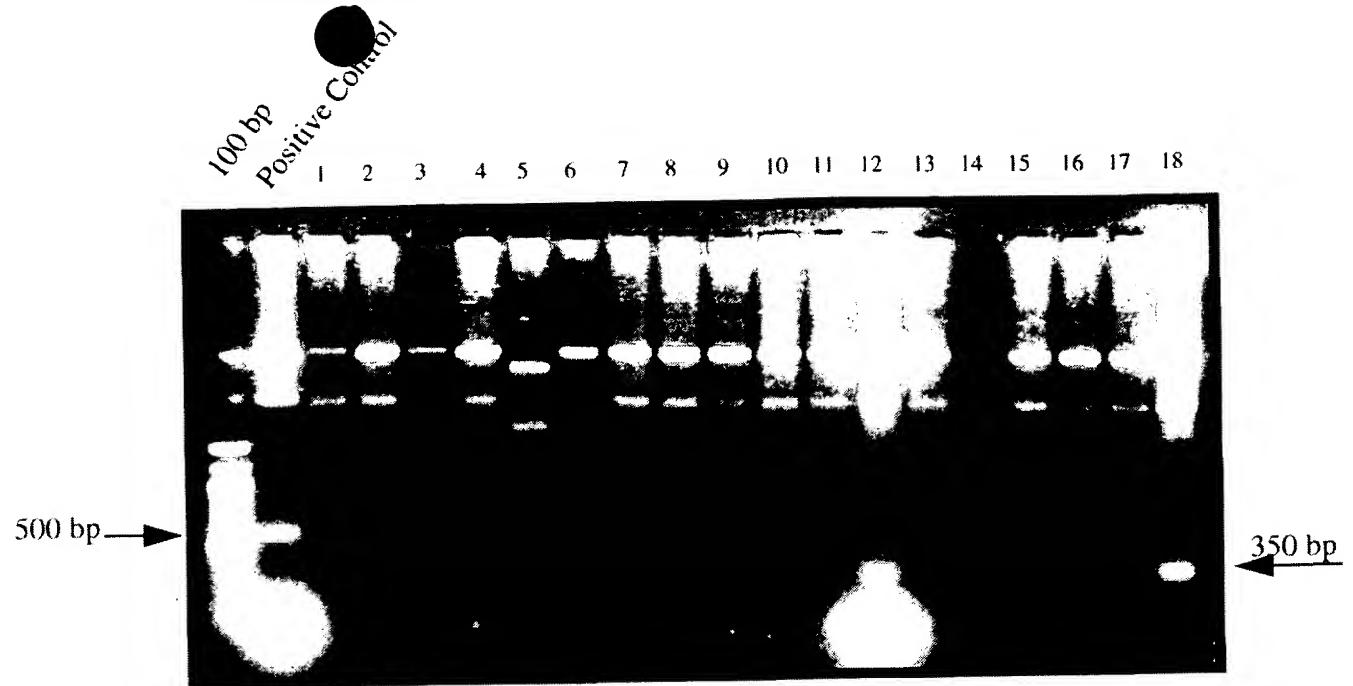


FIG. 5.2

TAE 2% PAGE - 0.0001

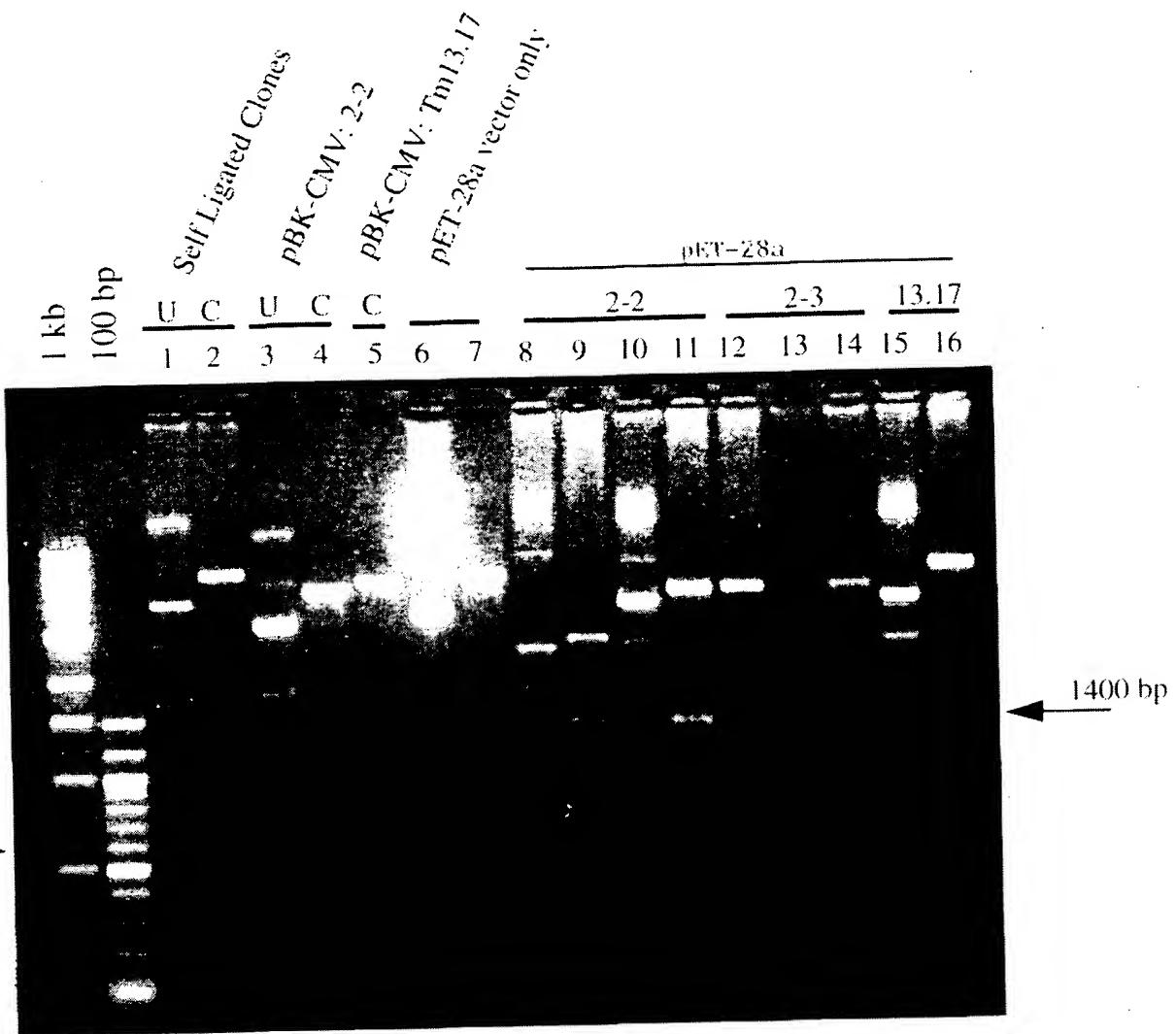


FIG. 5.3

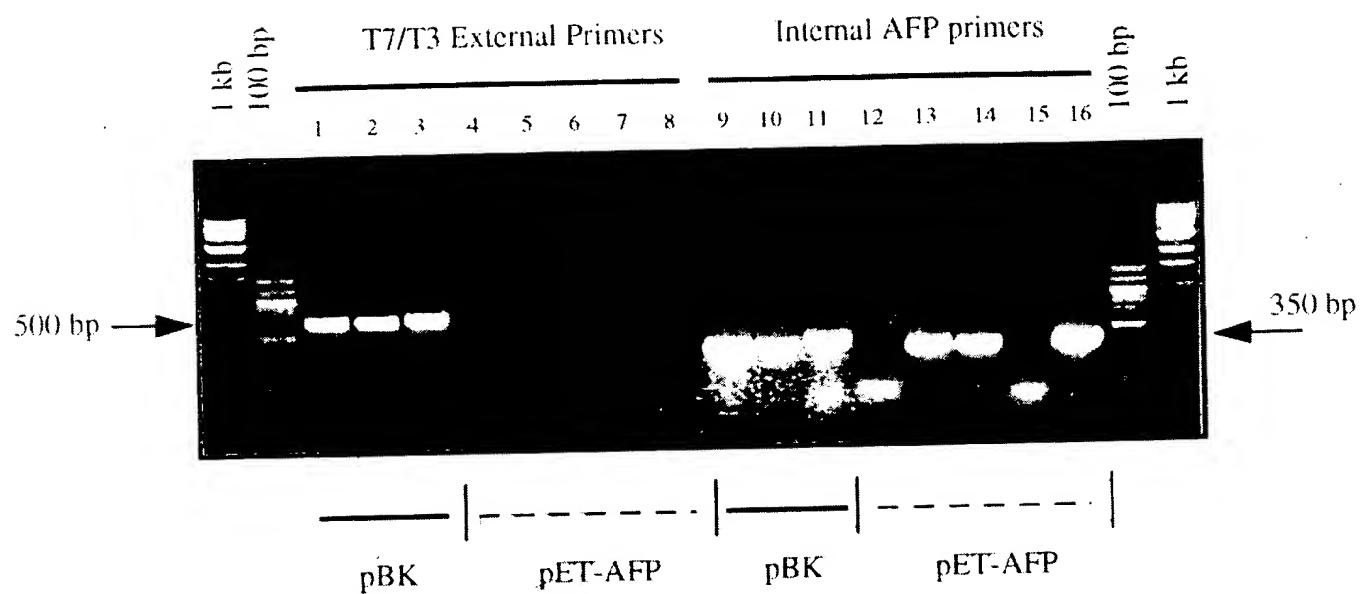
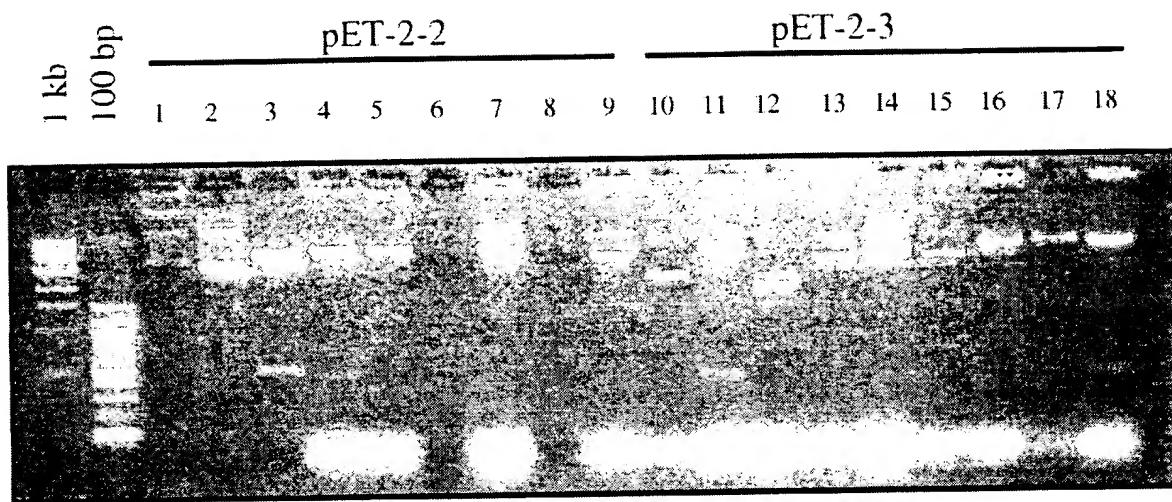
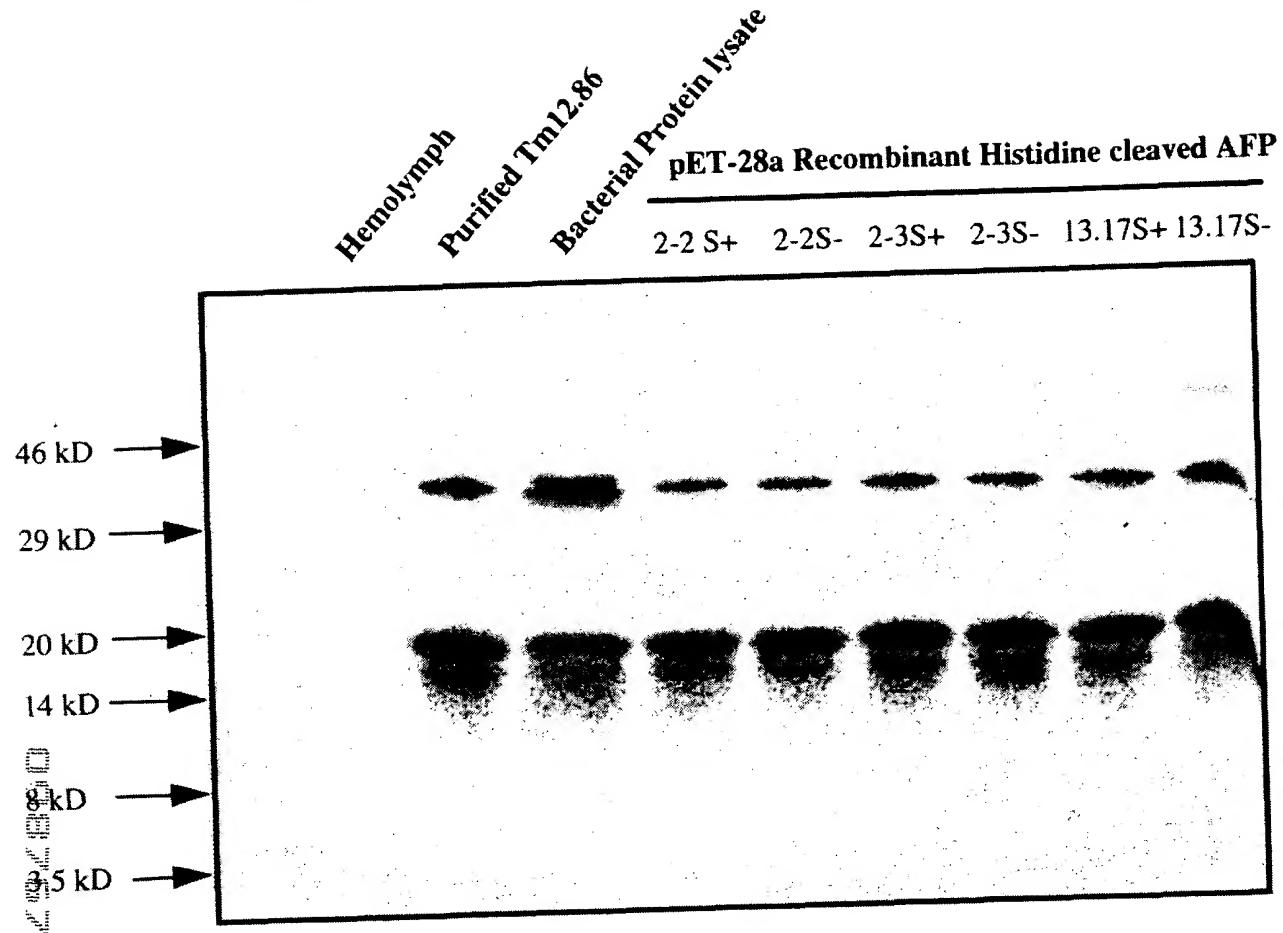


FIG. 5.4

7024090 "362660



**FIG. 5.5**



**FIG. 5.6**

His-tagged Clone 2.2 with signal sequence

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTGT TTACTTTAAG	50
His-tag Start Codon	
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC Met Gly Ser Ser His His His His His His Ser	96
-55 -50	
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	141
-45 -40 -35	
AFP Start Codon	
GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC GCA CGA GCA AAA ATG Gly Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys <u>Met</u>	186
-30 -25 -20	
AAA CTC CTC TTG TGC TTT GCG TTC GCC GCC ATC GTC ATC GGA GCT <u>Lys Leu Leu Cys Phe Ala Ala Ile Val Ile Gly Ala</u>	231
-15 -10 -5	
N-terminal of mature AFP	
CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA AGG AAC AAG ATC AGC <u>Gln Ala</u> Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser	276
1 5 10	
AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC CAA GAG ACG ATC GAC Lys Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp	321
15 20 25	
AAA GTC CGC ACA GGT GTC TTG GTC GAT GAT CCC AAA ATG AAG AAG Lys Val Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys	366
30 35 40	
CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA GTG GCA ACC GAA GCC His Val Leu Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala	411
45 50 55	
GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC AAG CTG AAG CAT GTG Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu Lys His Val	456
60 65 70	
GCC AGC GAC GAA GAG GTG GAC AAG ATC GTG CAG AAG TGC GTG GTC Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys Val Val	501
75 80 85	
AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT GAC ACC TTC AAG TGT Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys Cys	546
90 95 100	
Stop Codon	
ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT ATT GAT TAA TTGTTTGTA Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *	595
105 110 115	
Polyadenylation signal Poly-A tail	
TTTGACTGAA TTTTGACA <u>AT AAAGGTAATA</u> TCGTTATGTA AAAAAAAA	645
AAAAAAACTCG AGCACCAACC CCACCACAC TGAGAT	681

FIG. 5.7

His-tagged clone 2.2 without signal sequence

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTGT TTACTTTAAG	50
His-tag Start Codon	
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC	96*
Met Gly Ser Ser His His His His His His Ser	
-30	-25
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT	141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	
-20	-15
-10	
N-terminal of mature AFP	
GGA CAG CAA ATG GGT CGC GGA TCC CTC ACC GAC GAA CAG ATA CAG	186
Gly Gln Gln Met Gly Arg Gly Ser Leu Thr Asp Glu Gln Ile Gln	
-5	1
5	
AAA AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG	231
Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val	
10	15
20	
TCC CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAT	276
Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp	
25	30
35	
GAT CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT	321
Asp Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr	
40	45
50	
GGA GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA	366
Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys	
55	60
65	
GCC AAG CTG AAG CAT GTG GCC AGC GAC GAA GAG GTG GAC AAG ATC	411
Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile	
70	75
80	
GTG CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT	456
Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala	
85	90
95	
TAT GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT	501
Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser	
100	105
110	
Stop Codon	
CCT ATT GAT TAA CTCGAGCACC ACCACCACCA CCACTGAGAT	543
Pro Ile Asp *	
115	

FIG. 5.8

His-tagged clone 2.3 with signal sequence

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTGT TTACTTTAAG	50
His-tag Start Codon	
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC	96
Met Gly Ser Ser His His His His His His Ser	
-55	-50
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT	141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	
-45	-40
-35	
Gly Gln CAA ATG GGT CGC GGA TCC GAA TTC GCA CGA GCA AAA ATG	186
Gly Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys <u>Met</u>	
-30	-25
-20	
AFP Start Codon	
GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC GCA CGA GCA AAA ATG	186
Gly Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys <u>Met</u>	
-30	-25
-20	
AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC ATC GTC ATC GGA GCT	231
<u>Lys</u> Leu Leu Leu Cys Phe Ala Ala Ile Val Ile Gly Ala	
-15	-10
-5	
N-terminal of Mature AFP	
CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA AGG AAC AAG ATC AGC	276
<u>Gln</u> <u>Ala</u> Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser	
1	5
10	
AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC CAA GAG ACG ATC GAC	321
Lys Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp	
15	20
25	
AAA GTC CGC ACA GGT GTC TTG GTC GAT GAT CCC AAA ATG AAG AAG	366
Lys Val Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys	
30	35
40	
CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA GTG GCA ACC GAA GCC	411
His Val Leu Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala	
45	50
55	
GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC AAG CTG AAG CAT GTG	456
Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu Lys His Val	
60	65
70	
GCC AGC GAC GAA GAA GTG GAC AAG ATC GTG CAG AAG TGC GTG GTC	501
Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys Val Val	
75	80
85	
AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT GAC ACC TTC AAG TGT	546
Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys Cys	
90	95
100	
Stop Codon	
ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT ATT GAT TAA TTGTTTGTA	595
Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *	
105	110
115	
Polyadenylation signal	Poly-A tail
TTTGACTGAA TTTTGACA <u>AT</u> AAAGGTACTA TCGTTATGAA AAAAAAAA	645
AAAAAAAAACTC GAGCACCACC ACCACCACTA CTGAGAT	682

FIG. 5.9

His-tagged Clone 2.3 without signal sequence

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTGT TTACTTTAAG	50
His-tag Start Codon	
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC Met Gly Ser Ser His His His His His Ser	96
-30   -25	
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	141
-20   -15   -10	
N-terminal of mature AFP	
GGA CAG CAA ATG GGT CGC GGA TCC CTC ACC GAC GAA CAG ATA CAG Gly Gln Gln Met Gly Arg Gly Ser Leu Thr Asp Glu Gln Ile Gln	186
-5   1   5	
AAA AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val	231
10   15   20	
TCC CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAT Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp	276
25   30   35	
GAT CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT Asp Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr	321
40   45   50	
GGA GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys	366
55   60   65	
GCC AAG CTG AAG CAT GTG GCC AGC GAC GAA GAA GTG GAC AAG ATC Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile	411
70   75   80	
GTG CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala	456
85   90   95	
TAT GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser	501
100   105   110	
Stop Codon	
CCT ATT GAT TAA CTCGAGCACC ACCACCACCA CCACTGAGAT Pro Ile Asp *	543
115	

FIG. 5.10

His-tagged Tm 13.17 with signal sequence

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTGT TTACTTTAAG	50
His-tag Start Codon	
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC Met Gly Ser Ser His His His His His His Ser -65 -60 -55	96
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly -50 -45 -40	141
GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC TGG ATC CAA AGA ATT Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Trp Ile Gln Arg Ile -35 -30 -25	186
AFP Start Codon	
CGG CAC GAG ACT ACT AAG ATG AAG TTG CTC TGT TGT CTA ATC TCC Arg His Glu Thr Thr Lys <u>Met Lys Leu Leu Cys Cys Leu Ile Ser</u> -20 -15 -10	231
N-terminal of mature AFP	
CTC ATT CTG TTG GTC ACA GTT CAG GCC CTG ACC GAG GCA CAA ATT <u>Leu Ile Leu Leu Val Thr Val Gln Ala</u> Leu Thr Glu Ala Gln Ile -5 1 5	276
GAG AAA CTG AAC AAG ATC AGC AAA AAA TGT CAA AAT GAA AGT GGA Glu Lys Leu Asn Lys Ile Ser Lys Lys Cys Gln Asn Glu Ser Gly 10 15 20	321
GTG TCG CAA GAG ATC ATA ACC AAA GCT CGC AAC GGT GAC TGG GAG Val Ser Gln Glu Ile Ile Thr Lys Ala Arg Asn Gly Asp Trp Glu 25 30 35	366
GAC GAT CCT AAA CTG AAA CGC CAA GTT TTT TGC GTG GCC AGG AAC Asp Asp Pro Lys Leu Lys Arg Gln Val Phe Cys Val Ala Arg Asn 40 45 50	411
GCC GGT CTG GCC ACG GAA TCG GGA GAG GTG GTG GTC GAC GTG TTG Ala Gly Leu Ala Thr Glu Ser Gly Glu Val Val Val Asp Val Leu 55 60 65	456
AGG GAG AAG GTG AGG AAG GTC ACT GAC AAC GAC GAA GAA ACT GAG Arg Glu Lys Val Arg Lys Val Thr Asp Asn Asp Glu Glu Thr Glu 70 75 80	501
AAA ATC ATC AAT AAG TGC GCC GTC AAG AGA GAT ACT GTT GAA GAG Lys Ile Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val Glu Glu 85 90 95	546
ACG GTG TTC AAT ACT TTC AAA TGT GTC ATG AAA AAC AAG CCA AAG Thr Val Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro Lys 100 105 110	595
Stop Codon	
TTC TCA CCA GTT GAT TGA ACCACCACGA CTAGTAGATG GTTCAAATGG Phe Ser Pro Val Asp *	643
115	
Polyadenylation signal Poly-A tail	
TGTGCTTAC ATATAAA <u>AT</u> AAAGTGTTC TGATGTAAAA AAAAAAAA AAAAAAAAA AACTCGAGAG TATTCTAGAG CGGCCGCGGG CCCATCGTTT	693
TCCACCCCTC GAGCACCACC ACCACCACCA CTGAGAT	743
	777

FIG. 5.11

His-tagged Tm 13.17 without signal sequence

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTGT TTACTTTAAG	50	
His-tag Start Codon		
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC Met Gly Ser Ser His His His His His Ser	96	
-30	-25	
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	141	
-20	-15	-10
N-terminal of mature AFP		
GGA CAG CAA ATG GGT CGC GGC CTG ACC GAG GCA CAA ATT GAG AAA Gly Gln Gln Met Gly Arg Gly Leu Thr Glu Ala Gln Ile Glu Lys	186	
-5	1	5
CTG AAC AAG ATC AGC AAA AAA TGT CAA AAT GAA AGT GGA GTG TCG Leu Asn Lys Ile Ser Lys Lys Cys Gln Asn Glu Ser Gly Val Ser	231	
10	15	20
CAA GAG ATC ATA ACC AAA GCT CGC AAC GGT GAC TGG GAG GAC GAT Gln Glu Ile Ile Thr Lys Ala Arg Asn Gly Asp Trp Glu Asp Asp	276	
25	30	35
CCT AAA CTG AAA CGC CAA GTT TTT TGC GTG GCC AGG AAC GCC GGT Pro Lys Leu Lys Arg Gln Val Phe Cys Val Ala Arg Asn Ala Gly	321	
40	45	50
CTG GCC ACG GAA TCG GGA GAG GTG GTG GTC GAC GTG TTG AGG GAG Leu Ala Thr Glu Ser Gly Glu Val Val Val Asp Val Leu Arg Glu	366	
55	60	65
AAG GTG AGG AAG GTC ACT GAC AAC GAC GAA GAA ACT GAG AAA ATC Lys Val Arg Lys Val Thr Asp Asn Asp Glu Glu Thr Glu Lys Ile	411	
70	75	80
ATC AAT AAG TGC GCC GTC AAG AGA GAT ACT GTT GAA GAG ACG GTG Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val Glu Glu Thr Val	456	
85	90	95
TTC AAT ACT TTC AAA TGT GTC ATG AAA AAC AAG CCA AAG TTC TCA Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro Lys Phe Ser	501	
100	105	110
Stop Codon		
CCA GTT GAT TGA CTCGAGCACC ACCACCACCA CCACTGAGAT Pro Val Asp *	543	
115		

**FIG. 5.12**

094327956 • 0962761

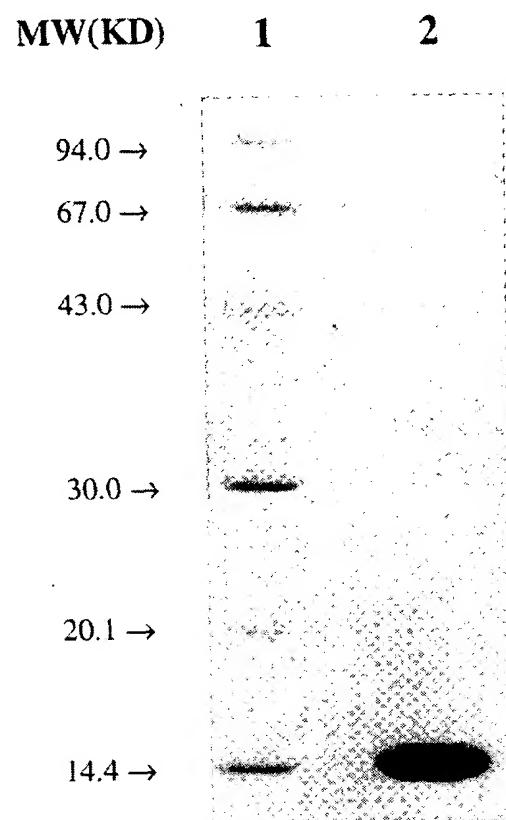


FIG. 6.0

FIGURE 6.1

1      2      3      MW(kb)

← 34.8

← 29.4

← 20.9

← 7.40

FIG. 6.1

09876796 "060704



FIG. 6.2

Tm 13.17 S- graph data

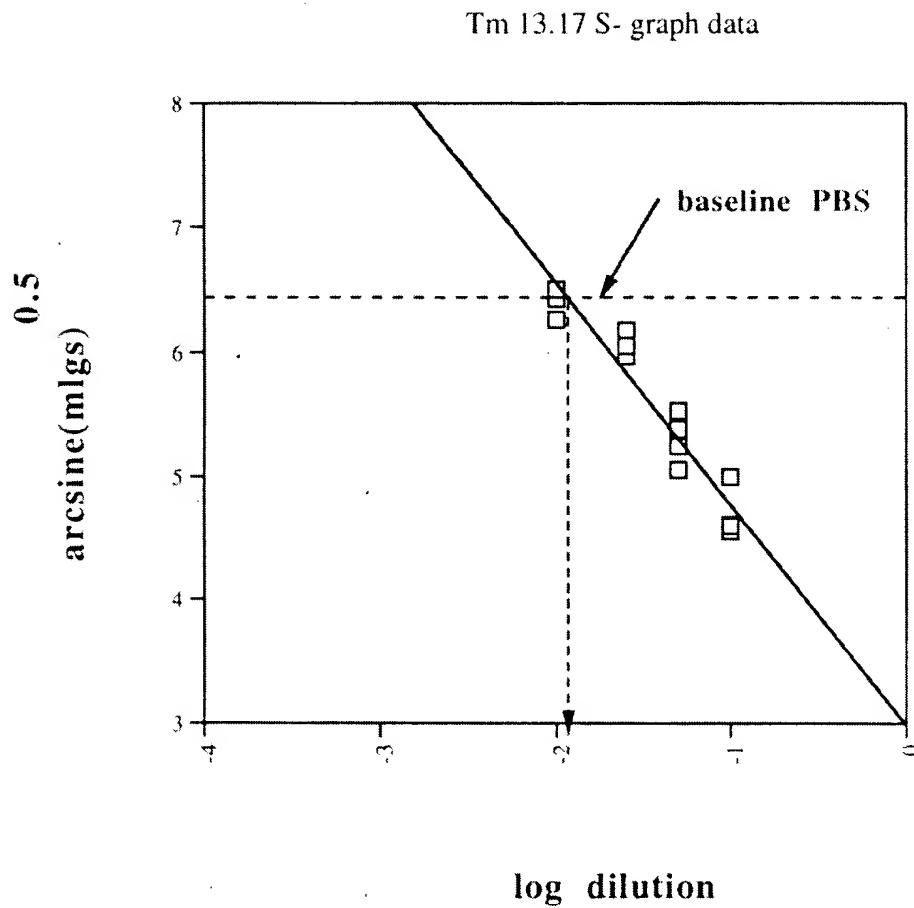


FIG. 6.3

P O Z D E S T E R

ONE LETTER	NAME	THREE LETTER	CHEMICAL CLASS	HYDROPHOBICITY	Reactivity
A	Alanine	Ala	aliphatic	mod. hydrophobic	low
B	Asp or Asn	Asx			
C	Cysteine	Cys	sulphydryl	hydrophobic	high
D	Aspartic Acid	Asp	acidic	highly hydrophilic	high
E	Glutamic Acid	Glu	acidic	highly hydrophilic	high
F	Phenylalanine	Phe	aromatic	highly hydrophobic	low
G	Glycine	Gly	aliphatic	mod. hydrophobic	low
H	Histidine	His	basic, imidazole	highly hydrophilic	high
I	Isoleucine	Ile	aliphatic	hydrophobic	low
J					
K	Lysine	Lys	basic	highly hydrophilic	high
L	Leucine	Leu	aliphatic	hydrophobic	low
M	Methionine	Met	sulphydryl	hydrophobic	low
N	Asparagine	Asn	amide, acidic derived	hydrophilic	high
O					
P	Proline	Pro	aliphatic, cyclic, imino	mod. hydrophilic	low
Q	Glutamine	Gln	amide, acidic derived	hydrophilic	high
R	Arginine	Arg	basic	highly hydrophilic	high
S	Serine	Ser	aliphatic hydroxyl	hydrophilic	high
T	Threonine	Thr	aliphatic hydroxyl	hydrophilic	high
U					
V	Valine	Val	aliphatic	hydrophobic	low
W	Tryptophan	Trp	aromatic	highly hydrophobic	low
X					
Y	Tyrosine	Tyr	aromatic	mod. hydrophilic	high
Z	Glu or Gln	Glx			
		ACD	Any Acidic		
		ALP	Any Aliphatic		
		ALH	Any Aliphatic Hydroxyl		
		ARO	Any Aromatic		
		BAS	Any Basic		
		HY-	Hydrophobic		
		HY+	Hydrophilic		

FIG. 7.1

□ □ □ □ □ □ □ □ □ □ □

Position	Tm 12.84-2.2	Tm 12.84-2.3	Tm 12.84-3.4	Tm 12.84-3.9	Tm 12.84-7.5	Consensus of Tm 12.84	Tm 13.17	Consensus with Tm 13.17	B1	Consensus with B1	AFP-3	Consensus with AFP-3
1	A	A	A	A	A	A	A	A		C	N	N
2	C	C	C	C	C	C	G	R		A	R	R
3	G	G	G	G	G	G	A	N		N	N	N
4	A	A	A	A	A	A	R	N		N	N	N
5	G	G	G	G	G	G	A	N		N	N	N
6	C	C	C	C	C	C	G	A		A	A	A
7	A	A	A	A	A	A	A	A		A	A	A
8	A	A	A	A	A	A	A	A		A	A	A
9	A	A	A	A	A	A	A	A		A	A	A
10	A	A	A	A	A	A	A	A		A	A	A
11	A	A	A	A	A	A	A	A		A	A	A
12	A	A	A	A	A	A	A	A		A	A	A
13	A	A	A	A	A	A	A	A		A	A	A
14	T	T	T	T	T	T	T	T		T	T	T
15	G	G	G	G	G	G	G	G		G	G	G
16	A	A	A	A	A	A	A	A		A	A	A
17	A	A	A	A	A	A	A	A		A	A	A
18	G	G	G	G	G	G	G	G		G	G	G
19	A	A	A	A	A	A	A	A		A	A	A
20	A	A	A	A	A	A	A	A		A	A	A
21	C	C	C	C	C	C	C	C		C	C	C
22	C	C	C	C	C	C	C	C		C	C	C
23	T	T	T	T	T	T	T	T		T	T	T
24	C	C	C	C	C	C	C	C		C	C	C
25	T	T	T	T	T	T	T	T		T	T	T
26	G	G	G	G	G	G	G	G		G	G	G
27	T	T	T	T	T	T	T	T		T	T	T
28	G	G	G	G	G	G	G	G		G	G	G
29	C	C	C	C	C	C	C	C		C	C	C
30	G	G	G	G	G	G	G	G		G	G	G
31	C	C	C	C	C	C	C	C		C	C	C
32	T	T	T	T	T	T	T	T		T	T	T
33	T	T	T	T	T	T	T	T		T	T	T
34	G	G	G	G	G	G	G	G		G	G	G
35	C	C	C	C	C	C	C	C		C	C	C
36	G	G	G	G	G	G	G	G		G	G	G
37	T	T	T	T	T	T	T	T		T	T	T
38	C	C	C	C	C	C	C	C		C	C	C
39	G	G	G	G	G	G	G	G		G	G	G
40	C	C	C	C	C	C	C	C		C	C	C
41	C	C	C	C	C	C	C	C		C	C	C
42	G	G	G	G	G	G	G	G		G	G	G
43	A	A	A	A	A	A	A	A		A	A	A
44	T	T	T	T	T	T	T	T		T	T	T
45	C	C	C	C	C	C	C	C		C	C	C
46	G	G	G	G	G	G	G	G		G	G	G
47	C	C	C	C	C	C	C	C		C	C	C
48	T	T	T	T	T	T	T	T		T	T	T
49	C	C	C	C	C	C	C	C		C	C	C
50	G	G	G	G	G	G	G	G		G	G	G
51	T	T	T	T	T	T	T	T		T	T	T
52	C	C	C	C	C	C	C	C		C	C	C
53	A	A	A	A	A	A	A	A		A	A	A
54	T	T	T	T	T	T	T	T		T	T	T
55	C	C	C	C	C	C	C	C		C	C	C
56	G	G	G	G	G	G	G	G		G	G	G
57	A	A	A	A	A	A	A	A		A	A	A
58	G	G	G	G	G	G	G	G		G	G	G
59	C	C	C	C	C	C	C	C		C	C	C
60	T	T	T	T	T	T	T	T		T	T	T
61	A	A	A	A	A	A	A	A		A	A	A
62	T	T	T	T	T	T	T	T		T	T	T
63	C	C	C	C	C	C	C	C		C	C	C
64	A	A	A	A	A	A	A	A		A	A	A
65	G	G	G	G	G	G	G	G		G	G	G
66	T	T	T	T	T	T	T	T		T	T	T
67	C	C	C	C	C	C	C	C		C	C	C
68	A	A	A	A	A	A	A	A		A	A	A
69	A	A	A	A	A	A	A	A		A	A	A
70	A	A	A	A	A	A	A	A		A	A	A
71	G	G	G	G	G	G	G	G		G	G	G
72	A	A	A	A	A	A	A	A		A	A	A
73	C	C	C	C	C	C	C	C		C	C	C
74	G	G	G	G	G	G	G	G		G	G	G
75	A	A	A	A	A	A	A	A		A	A	A
76	A	A	A	A	A	A	A	A		A	A	A
77	C	C	C	C	C	C	C	C		C	C	C
78	G	G	G	G	G	G	G	G		G	G	G
79	A	A	A	A	A	A	A	A		A	A	A
80	C	C	C	C	C	C	C	C		C	C	C
81	G	G	G	G	G	G	G	G		G	G	G
82	A	A	A	A	A	A	A	A		A	A	A
83	T	T	T	T	T	T	T	T		T	T	T
84	C	C	C	C	C	C	C	C		C	C	C
85	A	A	A	A	A	A	A	A		A	A	A
86	G	G	G	G	G	G	G	G		G	G	G
87	A	A	A	A	A	A	A	A		A	A	A
88	G	G	G	G	G	G	G	G		G	G	G
89	A	A	A	A	A	A	A	A		A	A	A
90	A	A	A	A	A	A	A	A		A	A	A
91	A	A	A	A	A	A	A	A		A	A	A
92	G	G	G	G	G	G	G	G		G	G	G
93	A	A	A	A	A	A	A	A		A	A	A
94	G	G	G	G	G	G	G	G		G	G	G
95	A	A	A	A	A	A	A	A		A	A	A
96	C	C	C	C	C	C	C	C		C	C	C
97	A	A	A	A	A	A	A	A		A	A	A
98	G	G	G	G	G	G	G	G		G	G	G
99	A	A	A	A	A	A	A	A		A	A	A
100	T	T	T	T	T	T	T	T		T	T	T
101	C	C	C	C	C	C	C	C		C	C	C
102	A	A	A	A	A	A	A	A		A	A	A
103	G	G	G	G	G	G	G	G		G	G	G
104	A	A	A	A	A	A	A	A		A	A	A
105	A	A	A	A	A	A	A	A		A	A	A
106	A	A	A	A	A	A	A	A		A	A	A
107	A	A	A	A	A	A	A	A		A	A	A
108	G	G	G	G	G	G	G	G		G	G	G
109	A	A	A	A	A	A	A	A		A	A	A
110	A	A	A	A	A	A	A	A		A	A	A
111	A	A	A	A	A	A	A	A		A	A	A
112	T	T	T	T	T	T	T	T		T	T	T
113	G	G	G	G	G	G	G	G		G	G	G
114	C	C	C	C	C	C	C	C		C	C	C
115	A	A	A	A	A	A	A	A		A	A	A
116	G	G	G	G	G	G	G	G		G	G	G
117	G	G	G	G	G	G	G	G		G	G	G

FIG. 7.2

## Sequence Data

Position	Tm 12.84-2.2	Tm 12.84-2.3	Tm 12.84-3.4	Tm 12.84-3.9	Tm 12.84-7.5	Consensus of	Tm 13.17	Consensus with	B1	Consensus with	AFP-3	Consensus with
119	C	C	C	C	C	C	A	N	A	N	G	N
120	A	G	A	G	G	G	T	N	C	T	C	N
121	G	G	G	G	G	G	G	G	G	G	G	G
122	T	T	T	T	T	T	T	R	R	R	T	A
123	G	G	G	G	G	G	T/A	A	A	A	C	T
124	T	T	T	T	T	T	T	T/A	A	A	C	T
125	C	C	C	C	C	C	G	C/G	G	G	G	T
126	G	G	G	G	G	G	T	Y	G	G	G	G
127	G	G	G	G	G	G	G	G	G	G	G	G
128	A	A	A	A	A	A	A	G	G	G	G	G
129	G	G	G	G	G	G	G	G	G	G	G	G
130	T	T	T	T	T	T	T	T	T	T	T	T
131	T	T	T	T	T	T	T	T	T	T	T	T
132	G	G	G	G	G	G	G	G	G	G	G	G
133	T	T	T	T	T	T	T	T	T	T	T	T
134	C	C	C	C	C	C	C	C	C	C	C	C
135	C	C	C	C	C	C	C	C	C	C	C	C
136	A	A	A	A	A	A	A	A	A	A	A	A
137	A	A	A	A	A	A	A	A	A	A	A	A
138	G	G	G	G	G	G	G	G	G	G	G	G
139	A	A	A	A	A	A	A	A	A	A	A	A
140	G	G	G	G	G	G	G	G	G	G	G	G
141	G	G	G	G	G	G	G	G	G	G	G	G
142	A	A	A	A	A	A	A	A	A	A	A	A
143	C	C	C	C	C	C	C	C	C	C	C	C
144	G	G	G	G	G	G	G	G	G	G	G	G
145	A	A	A	A	A	A	A	A	A	A	A	A
146	T	T	T	T	T	T	T	T	T	T	T	T
147	C	C	C	C	C	C	C	C	C	C	C	C
148	G	G	G	G	G	G	G	G	G	G	G	G
149	A	A	A	A	A	A	A	A	A	A	A	A
150	C	C	C	C	C	C	C	C	C	C	C	C
151	A	A	A	A	A	A	A	A	A	A	A	A
152	A	A	A	A	A	A	A	A	A	A	A	A
153	A	A	A	A	A	A	A	A	A	A	A	A
154	G	G	G	G	G	G	G	G	G	G	G	G
155	T	T	T	T	T	T	T	T	T	T	T	T
156	C	C	C	C	C	C	C	C	C	C	C	C
157	G	G	G	G	G	G	G	G	G	G	G	G
158	C	C	C	C	C	C	C	C	C	C	C	C
159	A	A	A	A	A	A	A	A	A	A	A	A
160	C	C	C	C	C	C	C	C	C	C	C	C
161	A	A	A	A	A	A	A	A	A	A	A	A
162	G	G	G	G	G	G	G	G	G	G	G	G
163	T	T	T	T	T	T	T	T	T	T	T	T
164	G	G	G	G	G	G	G	G	G	G	G	G
165	T	T	T	T	T	T	T	T	T	T	T	T
166	G	G	G	G	G	G	G	G	G	G	G	G
167	T	T	T	T	T	T	T	T	T	T	T	T
168	C	C	C	C	C	C	C	C	C	C	C	C
169	T	T	T	T	T	T	T	T	T	T	T	T
170	G	G	G	G	G	G	G	G	G	G	G	G
171	T	T	T	T	T	T	T	T	T	T	T	T
172	G	G	G	G	G	G	G	G	G	G	G	G
173	T	T	T	T	T	T	T	T	T	T	T	T
174	C	C	C	C	C	C	C	C	C	C	C	C
175	G	G	G	G	G	G	G	G	G	G	G	G
176	A	A	A	A	A	A	A	A	A	A	A	A
177	T	T	T	T	T	T	T	T	T	T	T	T
178	G	G	G	G	G	G	G	G	G	G	G	G
179	A	A	A	A	A	A	A	A	A	A	A	A
180	T	T	T	T	T	T	T	T	T	T	T	T
181	C	C	C	C	C	C	C	C	C	C	C	C
182	A	A	A	A	A	A	A	A	A	A	A	A
183	C	C	C	C	C	C	C	C	C	C	C	C
184	A	A	A	A	A	A	A	A	A	A	A	A
185	A	A	A	A	A	A	A	A	A	A	A	A
186	A	A	A	A	A	A	A	A	A	A	A	A
187	A	A	A	A	A	A	A	A	A	A	A	A
188	T	T	T	T	T	T	T	T	T	T	T	T
189	G	G	G	G	G	G	G	G	G	G	G	G
190	A	A	A	A	A	A	A	A	A	A	A	A
191	A	A	A	A	A	A	A	A	A	A	A	A
192	G	G	G	G	G	G	G	G	G	G	G	G
193	A	A	A	A	A	A	A	A	A	A	A	A
194	A	A	A	A	A	A	A	A	A	A	A	A
195	G	G	G	G	G	G	G	G	G	G	G	G
196	C	C	C	C	C	C	C	C	C	C	C	C
197	A	A	A	A	A	A	A	A	A	A	A	A
198	C	C	C	C	C	C	C	C	C	C	C	C
199	G	G	G	G	G	G	G	G	G	G	G	G
200	T	T	T	T	T	T	T	T	T	T	T	T
201	C	C	C	C	C	C	C	C	C	C	C	C
202	C	C	C	C	C	C	C	C	C	C	C	C
203	T	T	T	T	T	T	T	T	T	T	T	T
204	C	C	C	C	C	C	C	C	C	C	C	C
205	T	T	T	T	T	T	T	T	T	T	T	T
206	G	G	G	G	G	G	G	G	G	G	G	G
207	T	T	T	T	T	T	T	T	T	T	T	T
208	C	C	C	C	C	C	C	C	C	C	C	C
209	T	T	T	T	T	T	T	T	T	T	T	T
210	G	G	G	G	G	G	G	G	G	G	G	G
211	A	A	A	A	A	A	A	A	A	A	A	A
212	C	C	C	C	C	C	C	C	C	C	C	C
213	G	G	G	G	G	G	G	G	G	G	G	G
214	A	A	A	A	A	A	A	A	A	A	A	A
215	A	A	A	A	A	A	A	A	A	A	A	A
216	G	G	G	G	G	G	G	G	G	G	G	G
217	A	A	A	A	A	A	A	A	A	A	A	A
218	A	A	A	A	A	A	A	A	A	A	A	A
219	A	A	A	A	A	A	A	A	A	A	A	A
220	A	A	A	A	A	A	A	A	A	A	A	A
221	C	C	C	C	C	C	C	C	C	C	C	C
222	T	T	T	T	T	T	T	T	T	T	T	T
223	G	G	G	G	G	G	G	G	G	G	G	G
224	A	A	A	A	A	A	A	A	A	A	A	A
225	G	G	G	G	G	G	G	G	G	G	G	G
226	T	T	T	T	T	T	T	T	T	T	T	T
227	G	G	G	G	G	G	G	G	G	G	G	G
228	G	G	G	G	G	G	G	G	G	G	G	G
229	C	C	C	C	C	C	C	C	C	C	C	C
230	A	A	A	A	A	A	A	A	A	A	A	A
231	A	A	A	A	A	A	A	A	A	A	A	A
232	C	C	C	C	C	C	C	C	C	C	C	C
233	C	C	C	C	C	C	C	C	C	C	C	C
234	G	G	G	G	G	G	G	G	G	G	G	G
235	G	G	G	G	G	G	G	G	G	G	G	G

FIG. 7.2 Cont.

Top of 16S rRNA

Position	Tm 12.84-2.2	Tm 12.84-2.3	Tm 12.84-3.4	Tm 12.84-3.9	Tm 12.84-7.5	Consensus of	Tm 13.17	Consensus with	B1	Consensus with	AFP-3	Consensus with
236	A	A	A	A	A	A	A	A	A	A	C	N
237	A	A	G	G	G	G	T	A	A	C	C	N
238	G	G	G	G	G	G	C	T	N	A	G	G
239	C	C	C	C	C	C	G	G	C	G	T	T
240	C	C	C	C	C	C	G	G	G	G	G	G
241	G	G	G	G	G	G	G	G	G	G	G	G
242	A	A	A	A	A	A	A	A	A	A	A	A
243	G	G	G	G	G	G	A	A	A	A	A	A
244	A	A	A	A	A	A	G	G	A	A	A	A
245	A	A	A	A	A	A	G	G	A	A	A	A
246	C	C	C	C	C	C	G	G	A	A	A	A
247	A	A	A	A	A	A	G	G	A	A	A	A
248	C	C	C	C	C	C	G	G	A	A	A	A
249	C	C	C	C	C	C	G	G	A	A	A	A
250	A	A	A	A	A	A	G	G	A	A	A	A
251	A	A	A	A	A	A	G	G	A	A	A	A
252	T	T	T	T	T	T	G	G	N	N	N	N
253	G	T	T	G	G	G	T	T	G	G	G	G
254	T	G	T	G	G	G	T	T	G	G	G	G
255	G	G	A	G	G	G	T	T	G	G	G	G
256	A	A	A	A	A	A	G	G	A	A	A	A
257	G	G	G	G	G	G	G	G	R	R	R	R
258	G	G	G	G	G	G	G	G	R	R	R	R
259	G	G	G	G	G	G	G	G	R	R	R	R
260	T	T	T	T	T	T	T	T	R	R	R	R
261	A	A	A	A	A	A	T	T	R	R	R	R
262	C	T	T	C	C	C	T	T	R	R	R	R
263	C	A	A	A	A	A	C	C	R	R	R	R
264	A	A	A	A	A	A	C	C	R	R	R	R
265	A	A	A	A	A	A	C	C	R	R	R	R
266	A	A	A	A	A	A	C	C	R	R	R	R
267	A	A	A	A	A	A	C	C	R	R	R	R
268	G	G	G	G	G	G	C	C	R	R	R	R
269	C	C	C	C	C	C	C	C	R	R	R	R
270	C	C	C	C	C	C	C	C	R	R	R	R
271	A	A	A	A	A	A	C	C	R	R	R	R
272	G	G	G	G	G	G	C	C	R	R	R	R
273	C	C	C	C	C	C	C	C	R	R	R	R
274	G	C	C	C	C	C	C	C	R	R	R	R
275	T	T	T	T	T	T	T	T	R	R	R	R
276	G	A	A	A	A	A	A	A	R	R	R	R
277	A	A	A	A	A	A	A	A	R	R	R	R
278	G	G	G	G	G	G	G	G	R	R	R	R
279	C	C	C	C	C	C	C	C	R	R	R	R
280	C	C	C	C	C	C	C	C	R	R	R	R
281	A	T	T	C	T	T	T	T	R	R	R	R
282	T	G	T	G	T	G	T	T	R	R	R	R
283	G	G	G	G	G	G	G	G	R	R	R	R
284	C	C	C	C	C	C	C	C	R	R	R	R
285	G	G	G	G	G	G	G	G	R	R	R	R
286	C	C	C	C	C	C	C	C	R	R	R	R
287	C	C	C	C	C	C	C	C	R	R	R	R
288	C	C	C	C	C	C	C	C	R	R	R	R
289	A	A	A	A	A	A	A	A	R	R	R	R
290	G	G	G	G	G	G	G	G	R	R	R	R
291	C	C	C	C	C	C	C	C	R	R	R	R
292	C	C	C	C	C	C	C	C	R	R	R	R
293	C	C	C	C	C	C	C	C	R	R	R	R
294	G	G	G	G	G	G	G	G	R	R	R	R
295	A	A	A	A	A	A	A	A	R	R	R	R
296	C	C	C	C	C	C	C	C	R	R	R	R
297	G	G	G	G	G	G	G	G	R	R	R	R
298	G	G	G	G	G	G	G	G	R	R	R	R
299	A	A	A	A	A	A	A	A	R	R	R	R
300	A	A	A	A	A	A	A	A	R	R	R	R
301	G	G	G	G	G	G	G	G	R	R	R	R
302	A	A	A	A	A	A	A	A	R	R	R	R
303	G	G	G	G	G	G	G	G	R	R	R	R
304	G	G	G	G	G	G	G	G	R	R	R	R
305	T	T	T	T	T	T	T	T	R	R	R	R
306	G	G	G	G	G	G	G	G	R	R	R	R
307	G	G	G	G	G	G	G	G	R	R	R	R
308	A	A	A	A	A	A	A	A	R	R	R	R
309	C	C	C	C	C	C	C	C	R	R	R	R
310	A	A	A	A	A	A	A	A	R	R	R	R
311	A	A	A	A	A	A	A	A	R	R	R	R
312	G	G	G	G	G	G	G	G	R	R	R	R
313	A	A	A	A	A	A	A	A	R	R	R	R
314	T	T	T	T	T	T	T	T	R	R	R	R
315	C	C	C	C	C	C	C	C	R	R	R	R
316	G	G	G	G	G	G	G	G	R	R	R	R
317	T	T	T	T	T	T	T	T	R	R	R	R
318	G	G	G	G	G	G	G	G	R	R	R	R
319	C	C	C	C	C	C	C	C	R	R	R	R
320	A	A	A	A	A	A	A	A	R	R	R	R
321	G	G	G	G	G	G	G	G	R	R	R	R
322	A	A	A	A	A	A	A	A	R	R	R	R
323	A	A	A	A	A	A	A	A	R	R	R	R
324	G	G	G	G	G	G	G	G	R	R	R	R
325	T	T	T	T	T	T	T	T	R	R	R	R
326	G	G	G	G	G	G	G	G	R	R	R	R
327	C	C	C	C	C	C	C	C	R	R	R	R
328	G	G	G	G	G	G	G	G	R	R	R	R
329	T	T	T	T	T	T	T	T	R	R	R	R
330	G	G	G	G	G	G	G	G	R	R	R	R
331	G	G	G	G	G	G	G	G	R	R	R	R
332	T	T	T	T	T	T	T	T	R	R	R	R
333	C	C	C	C	C	C	C	C	R	R	R	R
334	A	A	A	A	A	A	A	A	R	R	R	R
335	A	A	A	A	A	A	A	A	R	R	R	R
336	G	G	G	G	G	G	G	G	R	R	R	R
337	A	A	A	A	A	A	A	A	R	R	R	R
338	A	A	A	A	A	A	A	A	R	R	R	R
339	G	G	G	G	G	G	G	G	R	R	R	R
340	G	G	G	G	G	G	G	G	R	R	R	R
341	C	C	C	C	C	C	C	C	R	R	R	R
342	C	C	C	C	C	C	C	C	R	R	R	R
343	A	A	A	A	A	A	A	A	R	R	R	R
344	C	C	C	C	C	C	C	C	R	R	R	R
345	A	A	A	A	A	A	A	A	R	R	R	R
346	C	C	C	C	C	C	C	C	R	R	R	R
347	C	C	C	C	C	C	C	C	R	R	R	R
348	A	A	A	A	A	A	A	A	R	R	R	R
349	G	G	G	G	G	G	G	G	R	R	R	R
350	A	A	A	A	A	A	A	A	R	R	R	R
351	G	G	G	G	G	G	G	G	R	R	R	R
352	G	G	G	G	G	G	G	G	R	R	R	R
353	A	A	A	A	A	A	A	A	R	R	R	R

FIG. 7.2 Cont.

Sequence Data

Position	Tm 12.84-2.2	Tm 12.84-2.3	Tm 12.84-3.4	Tm 12.84-3.9	Tm 12.84-7.5	Consensus of	Tm 13.17	Consensus with	B1	Consensus with	AFP-3	Consensus with
354	A	A	A	A	A	A	G	R	A	R	N	N
355	A	A	A	A	A	A	C	A	C	N	C/G	N
356	C	C	C	C	C	C	G	C	G	N	N	G/C
357	G	G	G	G	G	G	G	G	G	N	N	N
358	G	G	G	G	G	G	N	N	N	N	N	R
359	G	G	G	G	G	G	N	N	N	N	N	R
360	T	T	T	T	T	T	T	T	T	A	A	R
361	T	T	T	T	T	T	T	T	T	A	A	R
362	A	A	A	A	A	A	T	T	T	A	A	R
363	T	T	T	T	T	T	T	T	T	A	A	R
364	T	T	T	T	T	T	T	T	T	A	A	R
365	A	A	A	A	A	A	A	A	A	A	A	R
366	C	C	C	C	C	C	C	C	C	C	C	R
367	A	A	A	A	A	A	A	A	A	A	A	R
368	C	C	C	C	C	C	C	C	C	C	C	R
369	C	C	C	C	C	C	C	C	C	C	C	R
370	T	T	T	T	T	T	T	T	T	T	T	R
371	T	T	T	T	T	T	T	T	T	T	T	R
372	C	C	C	C	C	C	C	C	C	C	C	R
373	A	A	A	A	A	A	A	A	A	A	A	R
374	A	A	A	A	A	A	A	A	A	A	A	R
375	G	G	G	G	G	G	G	G	G	G	G	R
376	T	T	T	T	T	T	T	T	T	T	T	R
377	T	T	T	T	T	T	T	T	T	T	T	R
378	G	G	G	G	G	G	G	G	G	G	G	R
379	T	T	T	T	T	T	T	T	T	T	T	R
380	A	A	A	A	A	A	A	A	A	A	A	R
381	T	T	T	T	T	T	T	T	T	T	T	R
382	T	T	T	T	T	T	T	T	T	T	T	R
383	A	A	A	A	A	A	A	A	A	A	A	R
384	C	C	C	C	C	C	C	C	C	C	C	R
385	G	G	G	G	G	G	G	G	G	G	G	R
386	C	C	C	C	C	C	C	C	C	C	C	R
387	A	A	A	A	A	A	A	A	A	A	A	R
388	G	G	G	G	G	G	G	G	G	G	G	R
389	G	G	G	G	G	G	G	G	G	G	G	R
390	C	C	C	C	C	C	C	C	C	C	C	R
391	A	A	A	A	A	A	A	A	A	A	A	R
392	A	A	A	A	A	A	A	A	A	A	A	R
393	A	A	A	A	A	A	A	A	A	A	A	R
394	A	A	A	A	A	A	A	A	A	A	A	R
395	C	C	C	C	C	C	C	C	C	C	C	R
396	C	C	C	C	C	C	C	C	C	C	C	R
397	T	T	T	T	T	T	T	T	T	T	T	R
398	G	G	G	G	G	G	G	G	G	G	G	R
399	A	A	A	A	A	A	A	A	A	A	A	R
400	T	T	T	T	T	T	T	T	T	T	T	R
401	T	T	T	T	T	T	T	T	T	T	T	R
402	C	C	C	C	C	C	C	C	C	C	C	R
403	A	A	A	A	A	A	A	A	A	A	A	R
404	T	T	T	T	T	T	T	T	T	T	T	R
405	T	T	T	T	T	T	T	T	T	T	T	R
406	C	C	C	C	C	C	C	C	C	C	C	R
407	T	T	T	T	T	T	T	T	T	T	T	R
408	T	T	T	T	T	T	T	T	T	T	T	R
409	A	A	A	A	A	A	A	A	A	A	A	R
410	T	T	T	T	T	T	T	T	T	T	T	R
411	T	T	T	T	T	T	T	T	T	T	T	R
412	G	G	G	G	G	G	G	G	G	G	G	R
413	A	A	A	A	A	A	A	A	A	A	A	R
414	T	T	T	T	T	T	T	T	T	T	T	R
415	T	T	T	T	T	T	T	T	T	T	T	R
416	C	C	C	C	C	C	C	C	C	C	C	R
417	T	T	T	T	T	T	T	T	T	T	T	R
418	T	T	T	T	T	T	T	T	T	T	T	R
419	A	A	A	A	A	A	A	A	A	A	A	R
420	T	T	T	T	T	T	T	T	T	T	T	R
421	T	T	T	T	T	T	T	T	T	T	T	R
422	C	C	C	C	C	C	C	C	C	C	C	R
423	A	A	A	A	A	A	A	A	A	A	A	R
424	T	T	T	T	T	T	T	T	T	T	T	R
425	T	T	T	T	T	T	T	T	T	T	T	R
426	G	G	G	G	G	G	G	G	G	G	G	R
427	A	A	A	A	A	A	A	A	A	A	A	R
428	T	T	T	T	T	T	T	T	T	T	T	R
429	T	T	T	T	T	T	T	T	T	T	T	R
430	C	C	C	C	C	C	C	C	C	C	C	R
431	A	A	A	A	A	A	A	A	A	A	A	R
432	T	T	T	T	T	T	T	T	T	T	T	R
433	T	T	T	T	T	T	T	T	T	T	T	R
434	G	G	G	G	G	G	G	G	G	G	G	R
435	A	A	A	A	A	A	A	A	A	A	A	R
436	T	T	T	T	T	T	T	T	T	T	T	R
437	T	T	T	T	T	T	T	T	T	T	T	R
438	C	C	C	C	C	C	C	C	C	C	C	R
439	A	A	A	A	A	A	A	A	A	A	A	R
440	T	T	T	T	T	T	T	T	T	T	T	R
441	T	T	T	T	T	T	T	T	T	T	T	R
442	A	A	A	A	A	A	A	A	A	A	A	R
443	T	T	T	T	T	T	T	T	T	T	T	R
444	G	G	G	G	G	G	G	G	G	G	G	R
445	A	A	A	A	A	A	A	A	A	A	A	R
446	T	T	T	T	T	T	T	T	T	T	T	R
447	T	T	T	T	T	T	T	T	T	T	T	R
448	G	G	G	G	G	G	G	G	G	G	G	R
449	A	A	A	A	A	A	A	A	A	A	A	R
450	T	T	T	T	T	T	T	T	T	T	T	R
451	T	T	T	T	T	T	T	T	T	T	T	R
452	C	C	C	C	C	C	C	C	C	C	C	R
453	A	A	A	A	A	A	A	A	A	A	A	R
454	T	T	T	T	T	T	T	T	T	T	T	R
455	T	T	T	T	T	T	T	T	T	T	T	R
456	C	C	C	C	C	C	C	C	C	C	C	R
457	A	A	A	A	A	A	A	A	A	A	A	R
458	T	T	T	T	T	T	T	T	T	T	T	R
459	G	G	G	G	G	G	G	G	G	G	G	R
460	A	A	A	A	A	A	A	A	A	A	A	R
461	T	T	T	T	T	T	T	T	T	T	T	R
462	T	T	T	T	T	T	T	T	T	T	T	R
463	C	C	C	C	C	C	C	C	C	C	C	R
464	A	A	A	A	A	A	A	A	A	A	A	R
465	T	T	T	T	T	T	T	T	T	T	T	R
466	T	T	T	T	T	T	T	T	T	T	T	R
467	G	G	G	G	G	G	G	G	G	G	G	R
468	A	A	A	A	A	A	A	A	A	A	A	R
469	T	T	T	T	T	T	T	T	T	T	T	R
470	T	T	T	T	T	T	T	T	T	T	T	R
471	G	G	G	G	G	G	G	G	G	G	G	R

FIG. 7.2 Cont.

Position	Tm 12.84-2.2	Tm 12.84-2.3	Tm 12.84-3.4	Tm 12.84-3.9	Tm 12.84-7.5	Consensus of	Tm13.17	Consensus with	B1	Consensus with	AFP-3	Consensus with
472	A	A	A	A	A	A	A	A	A	A	A	A
473	A	A	A	A	A	A	A	A	A	A	A	A
474	T	T	T	T	T	T	T	T	T	T	T	T
475	A	A	A	A	A	A	A	A	A	A	A	A
476	A	A	A	A	A	A	A	A	A	A	A	A
477	A	A	A	A	A	A	A	A	A	A	A	A
478	G	G	G	G	G	G	G	G	G	G	T	N
479	G	G	G	G	G	G	G	G	G	N	T	N
480	T	T	T	T	T	T	T	T	N	N	A	N
481	A	A	C	A	C	A	C	T	Y	Y	A	A/T
482	A	T	T	T	T	T	T	T	T	T	A	A/T
483	A	A	T	A	T	T	T	C	T	T	G	A/T
484	A	A	T	T	T	T	T	T	N	R	A	A/T
485	T	C	T	C	C	G	C	G	R	T	A	T/A
486	C	G	T	G	T	G	T	G	R	N	R	R
487	G	T	T	T	T	T	T	G	T	N	N	N
488	T	T	T	T	T	T	T	G	N	N	A	A
489	A	T	T	T	T	T	T	A	R	N	A	A
490	A	T	T	T	T	T	T	A	A	A	A	A
491	T	G	T	T	G	G	T	G	A	A	A	A
492	G	A	A	T	A	A	A	A	A	A	A	A
493	T	A	A	A	A	A	A	A	A	R	A	A
494	A	A	A	A	A	A	A	A	A	A	A	A
495	A	A	A	A	A	A	A	A	A	A	A	A
496	A	A	A	A	A	A	A	A	A	A	A	A
497	A	A	A	A	A	A	A	A	A	A	A	A
498	A	A	A	A	A	A	A	A	A	A	A	A
499	A	A	A	A	A	A	A	A	A	A	A	A
500	A	A	A	A	A	A	A	A	A	A	A	A
501	A	A	A	A	A	A	A	A	A	A	A	A
502	A	A	A	A	A	A	A	A	A	A	A	A
503	A	A	A	A	A	A	A	A	A	A	A	A
504	A	A	A	A	A	A	A	A	A	A	A	A
505	A	A	A	A	A	A	A	A	A	A	A	A
506	A	A	A	A	A	A	A	A	A	A	A	A
507	A	A	A	A	A	A	A	A	A	A	A	A
508	A	A	A	A	A	A	A	A	A	A	A	A
509	A	A	A	A	A	A	A	A	A	A	A	A
510	A	A	A	A	A	A	A	A	A	A	A	A
511	A	A	A	A	A	A	A	A	A	A	A	A
512	A	A	A	A	A	A	A	A	A	A	A	A

FIG. 7.2 Cont.

FIG. 7.3

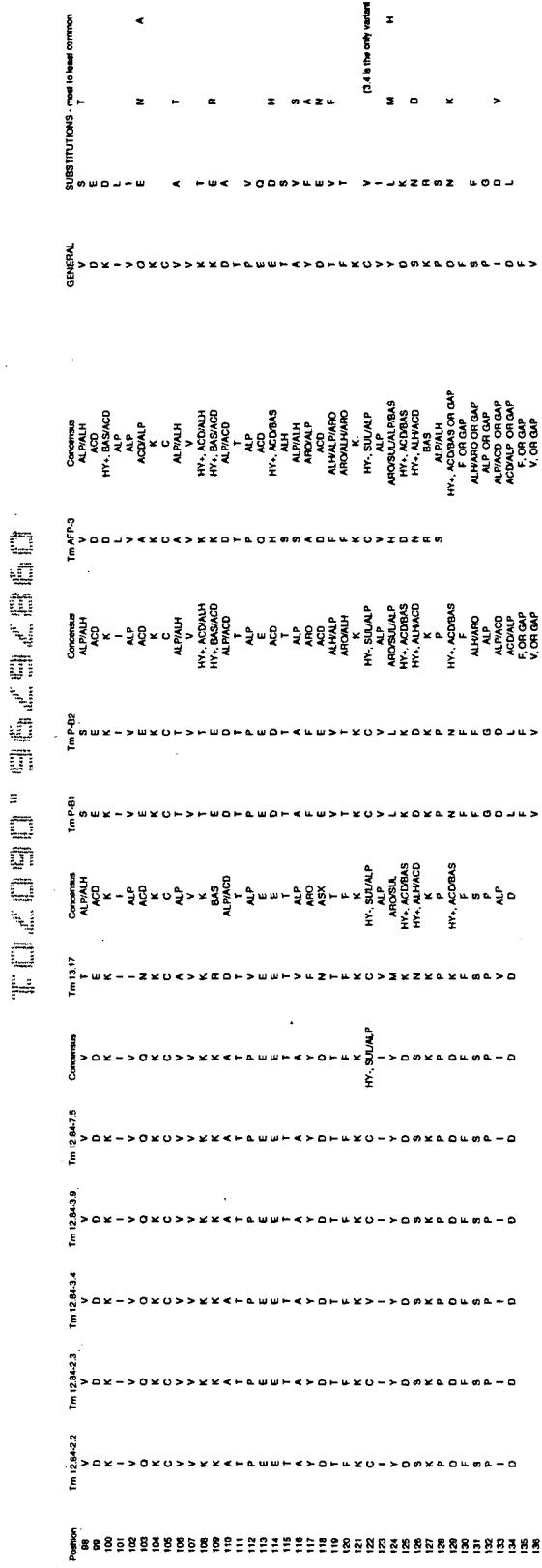


FIG. 7.3 Cont.

09637696 - 060201

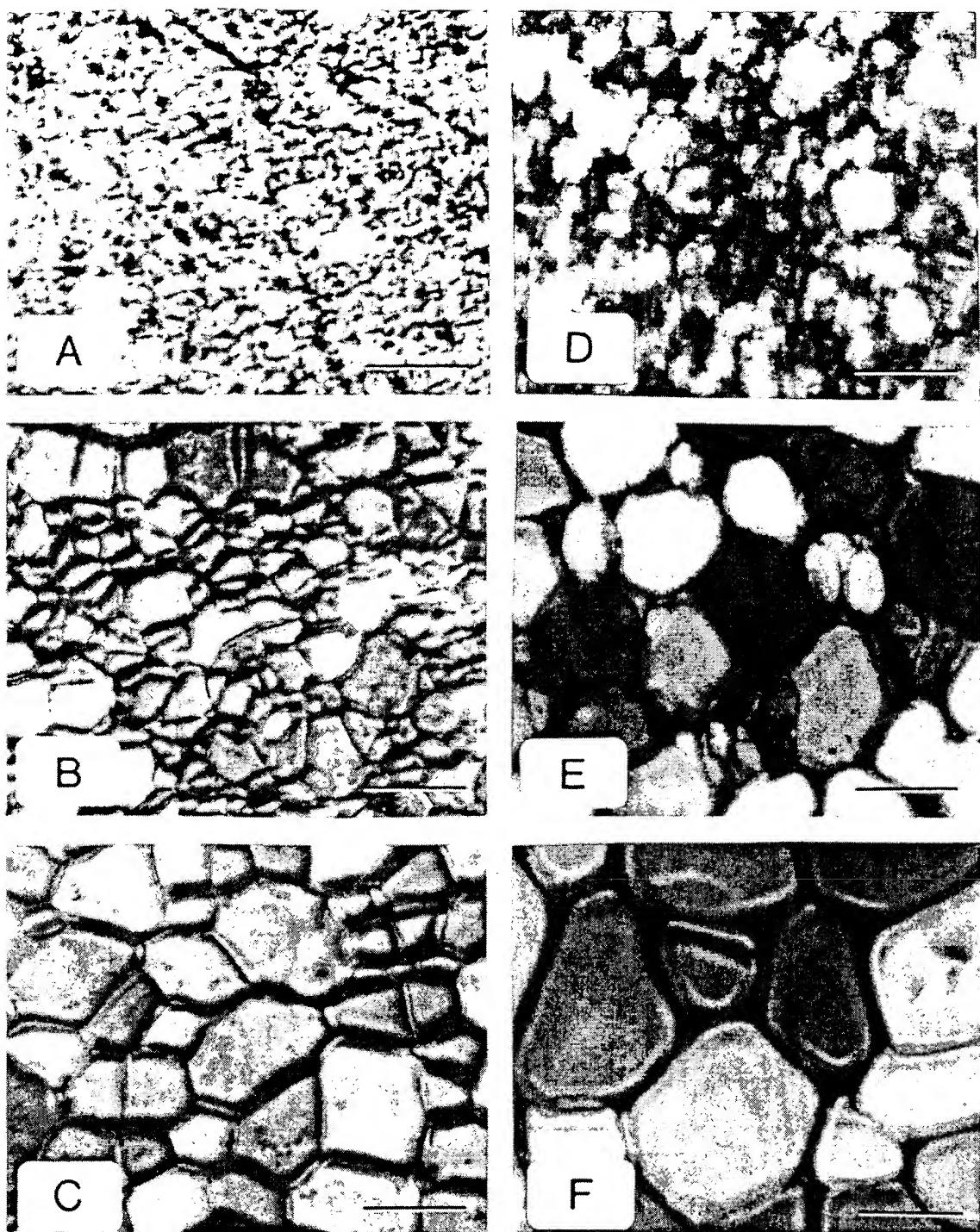
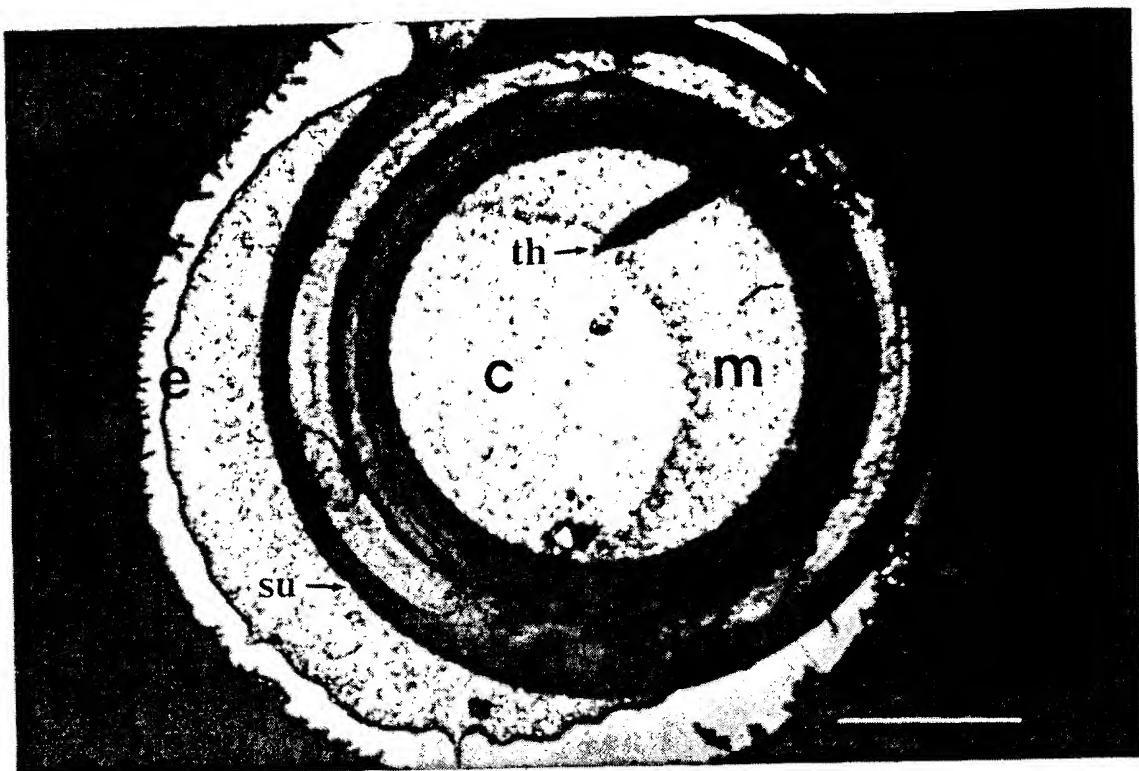
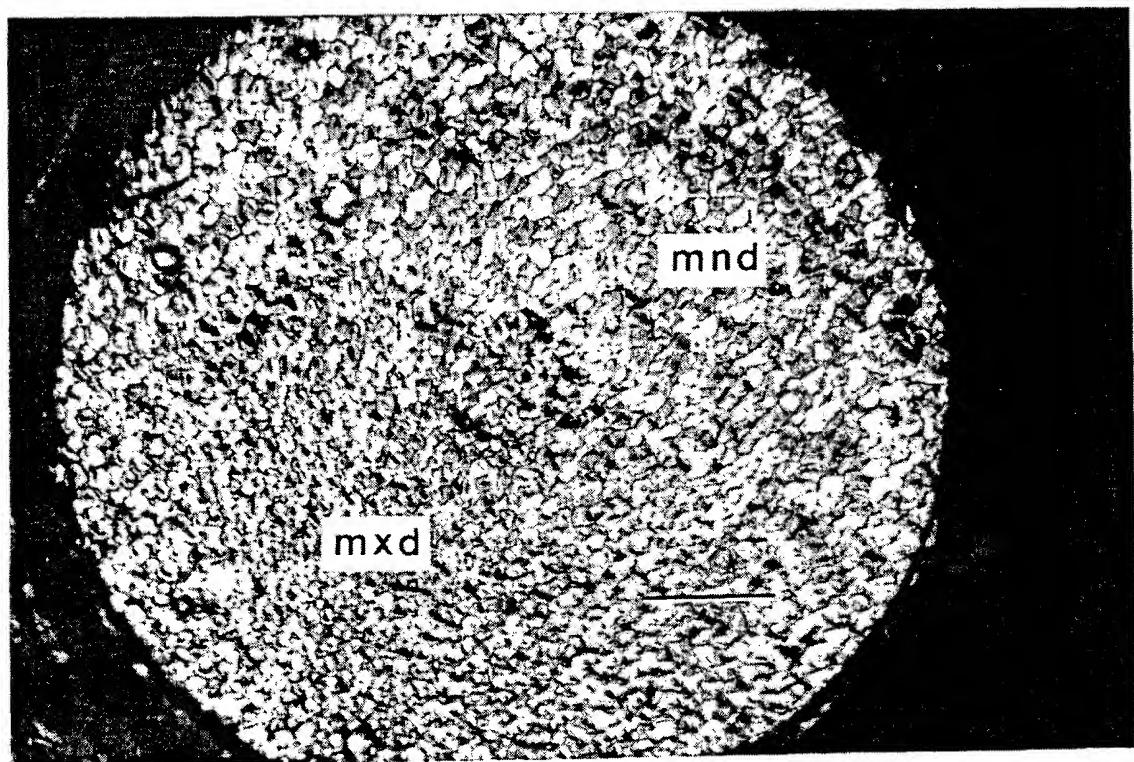


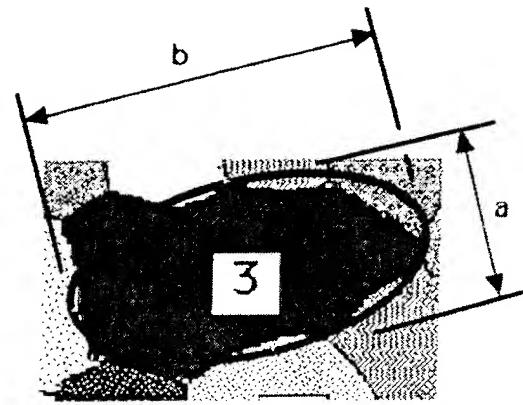
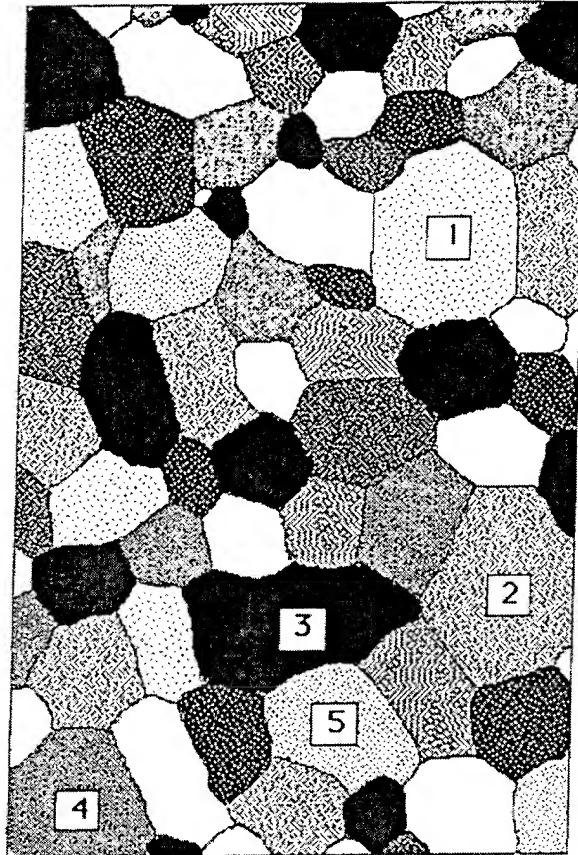
FIG. 8.0



**FIG. 8.1a**



**FIG. 8.1b**



grain area=0.25mm<sup>2</sup>

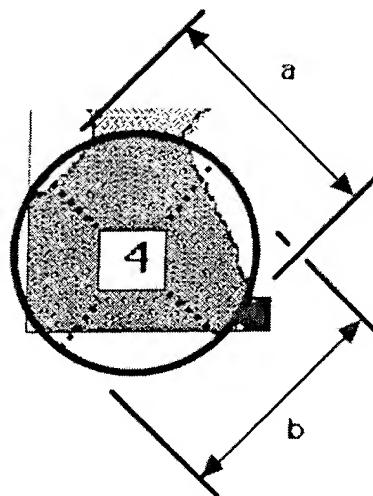


FIG. 8.2

06/26/2000

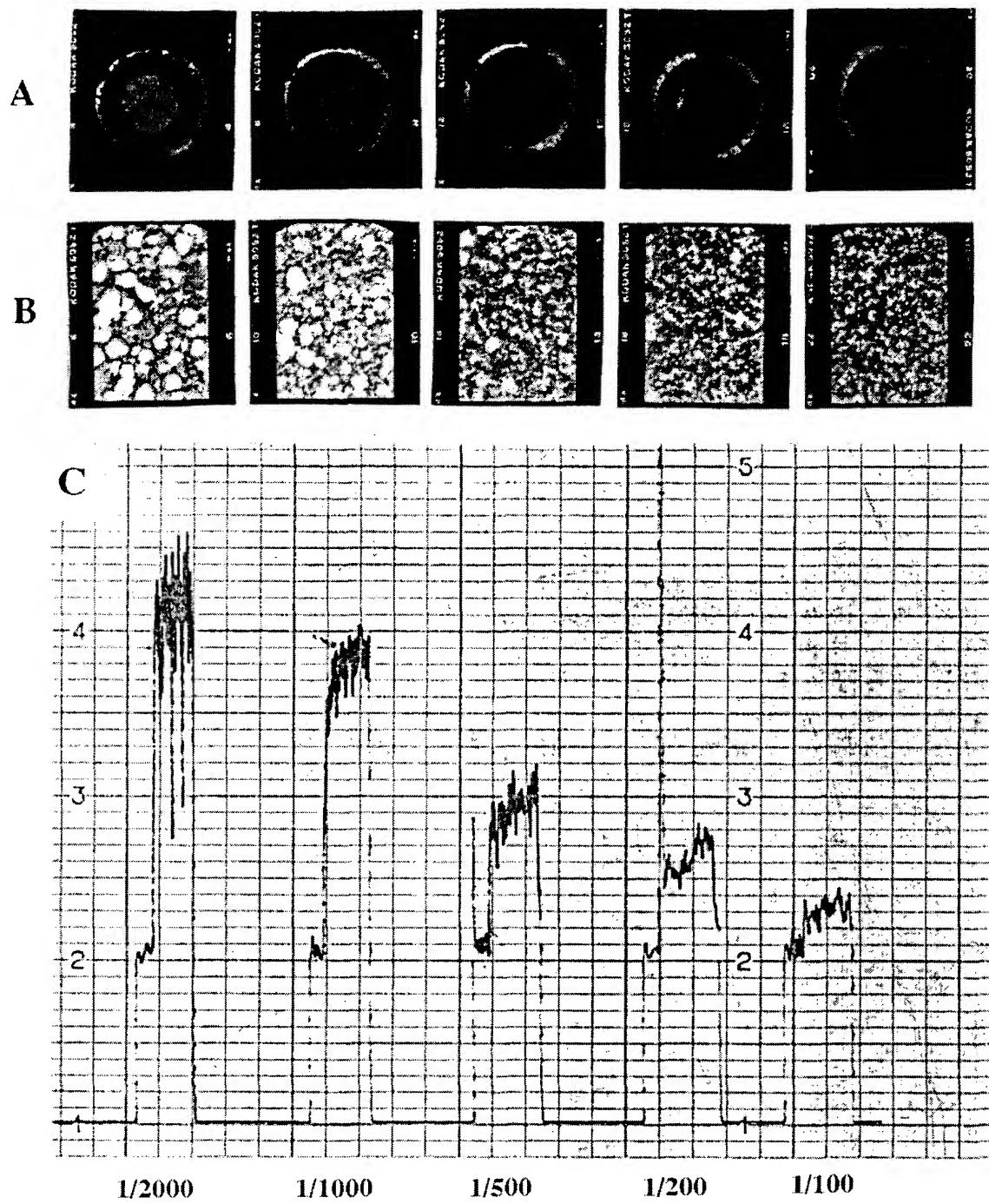


FIG. 8.3

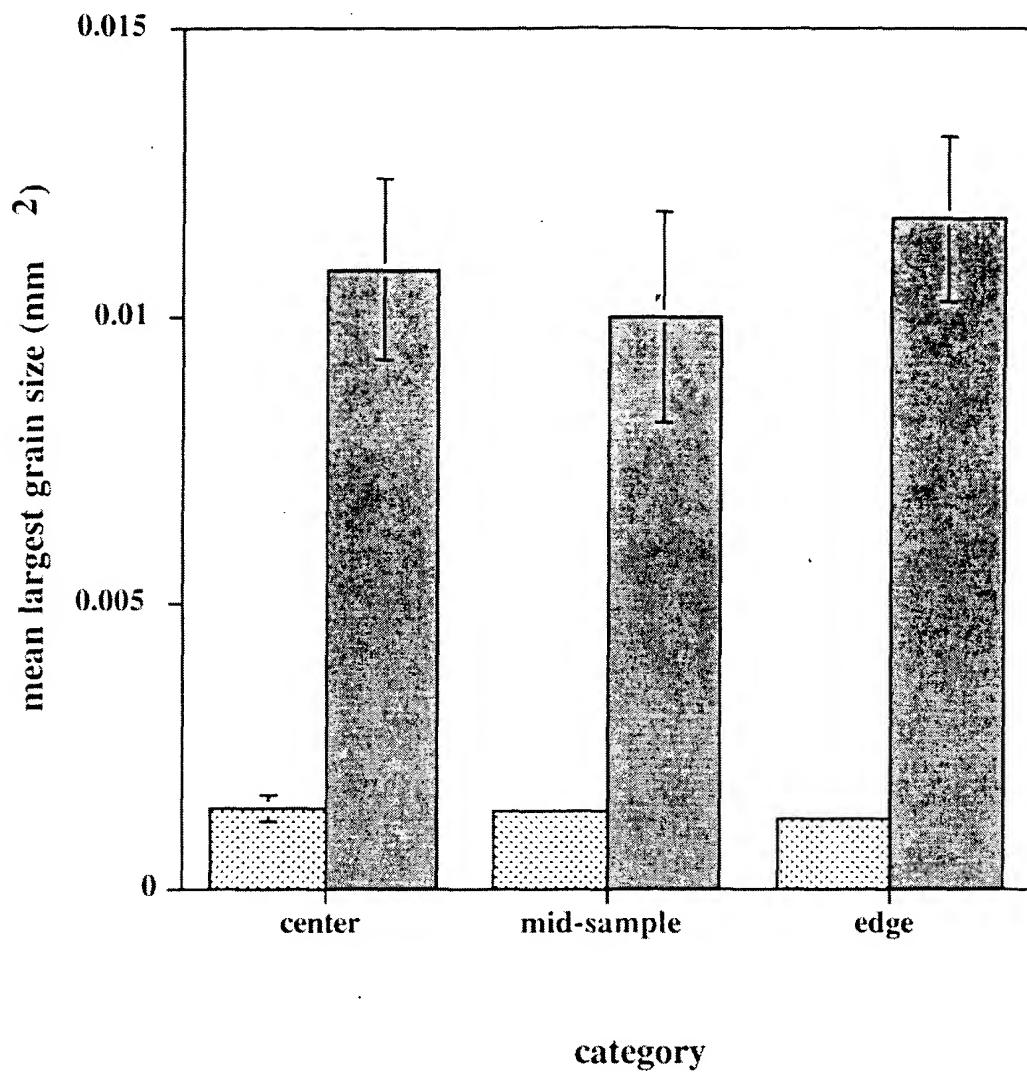


FIG. 8.4a

0987654321

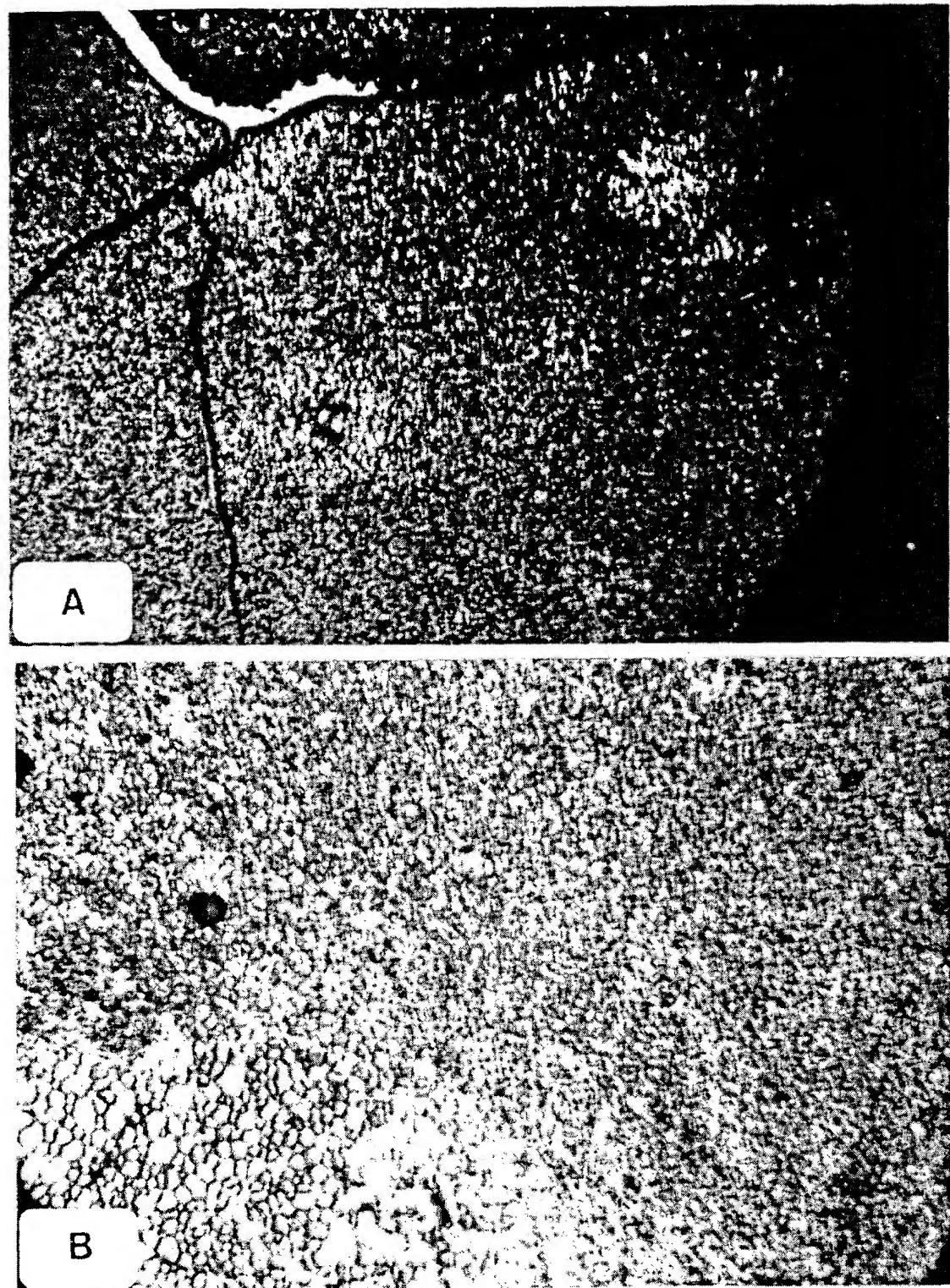


FIG. 8.4b

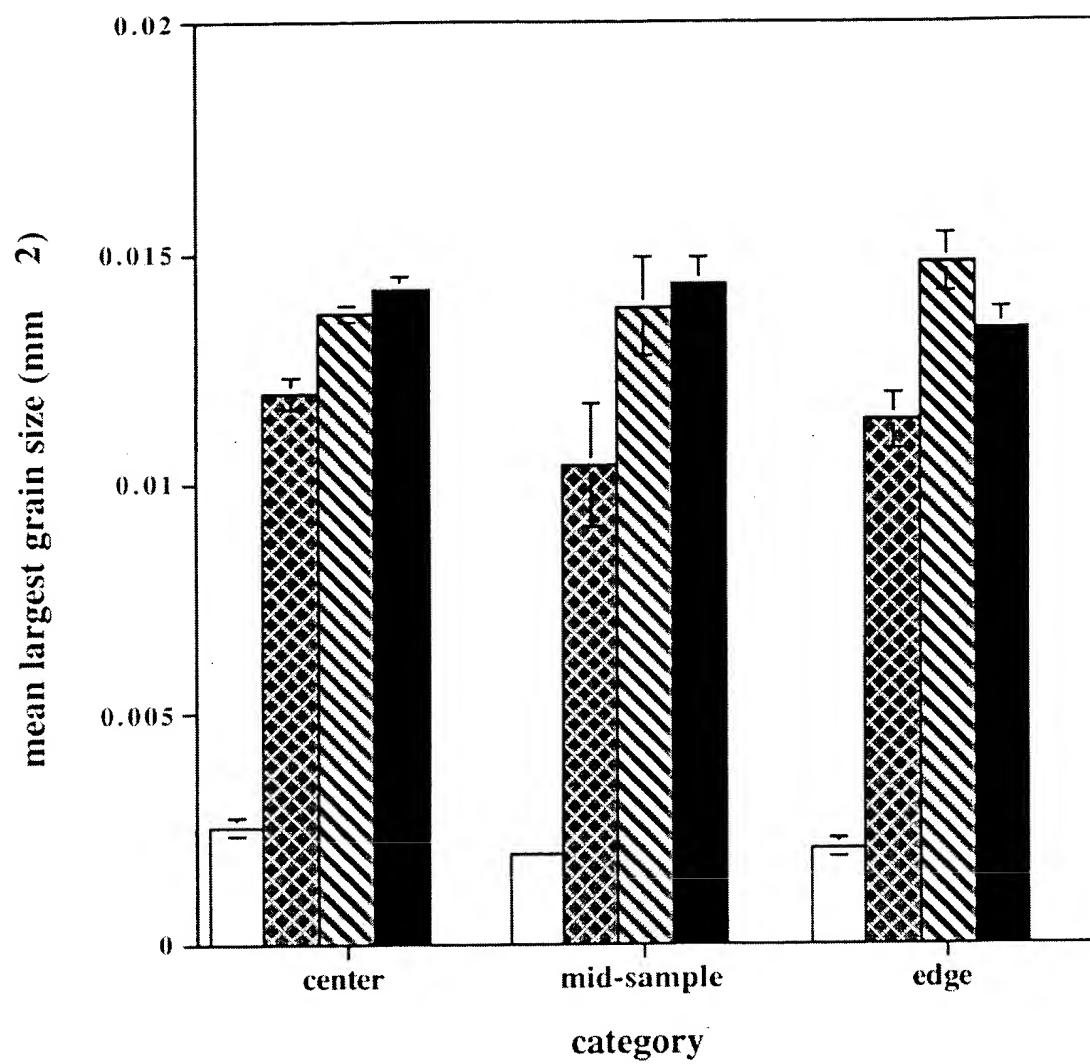
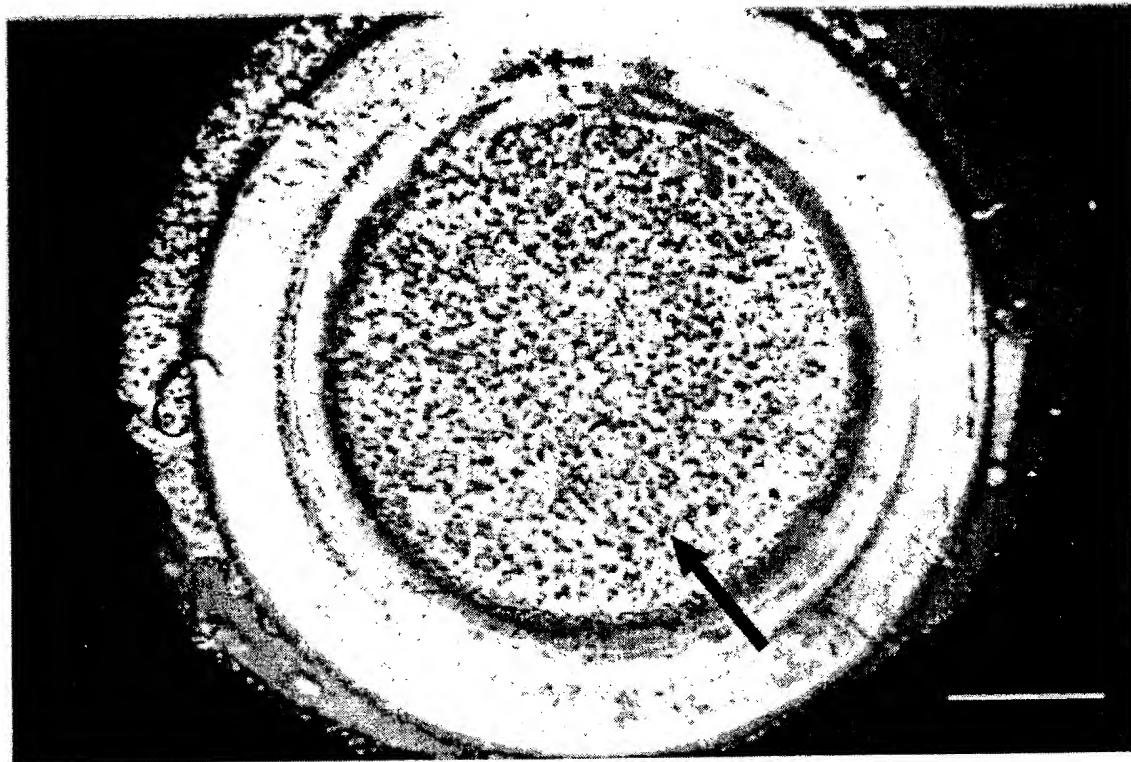


FIG. 8.5a

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**FIG. 8.5b**

04826296 "E0D0

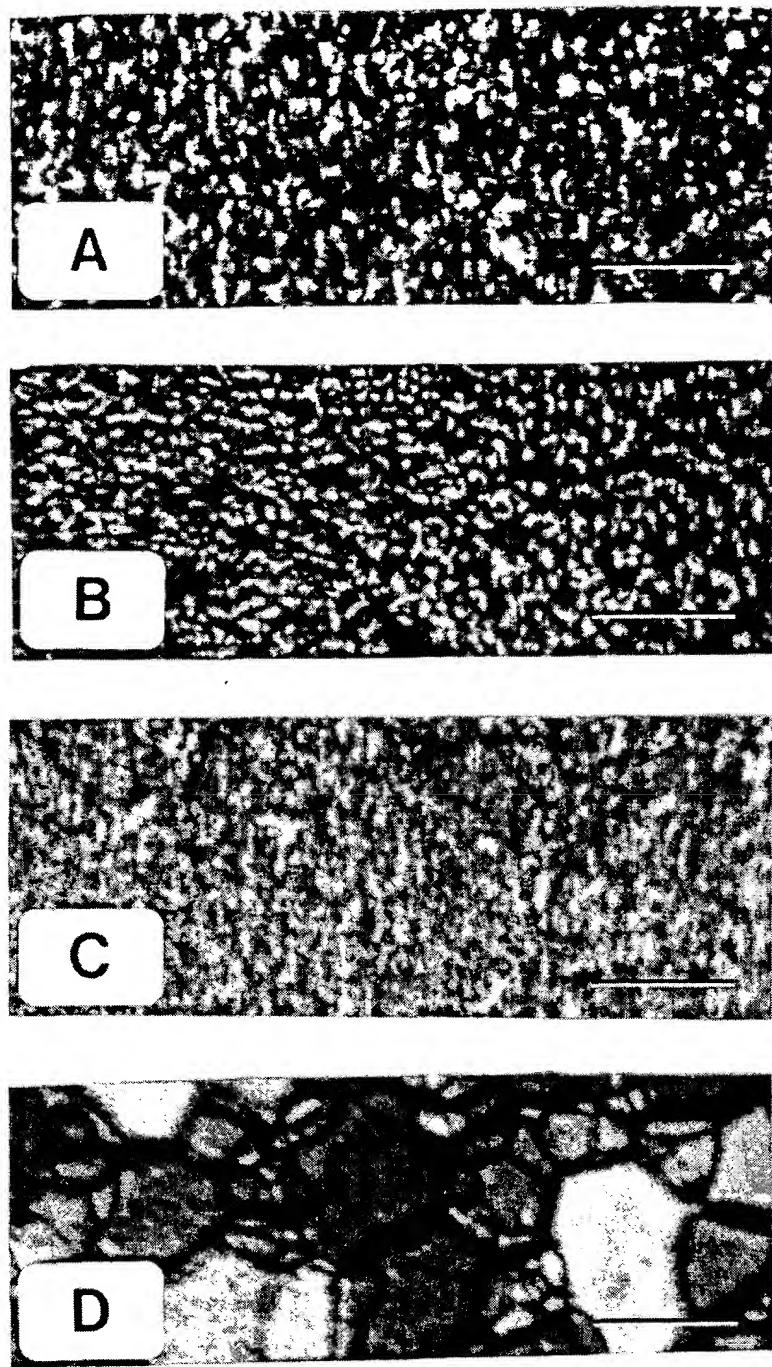


FIG. 8.6

FIGURE 8.7 - FIGURE 8.7

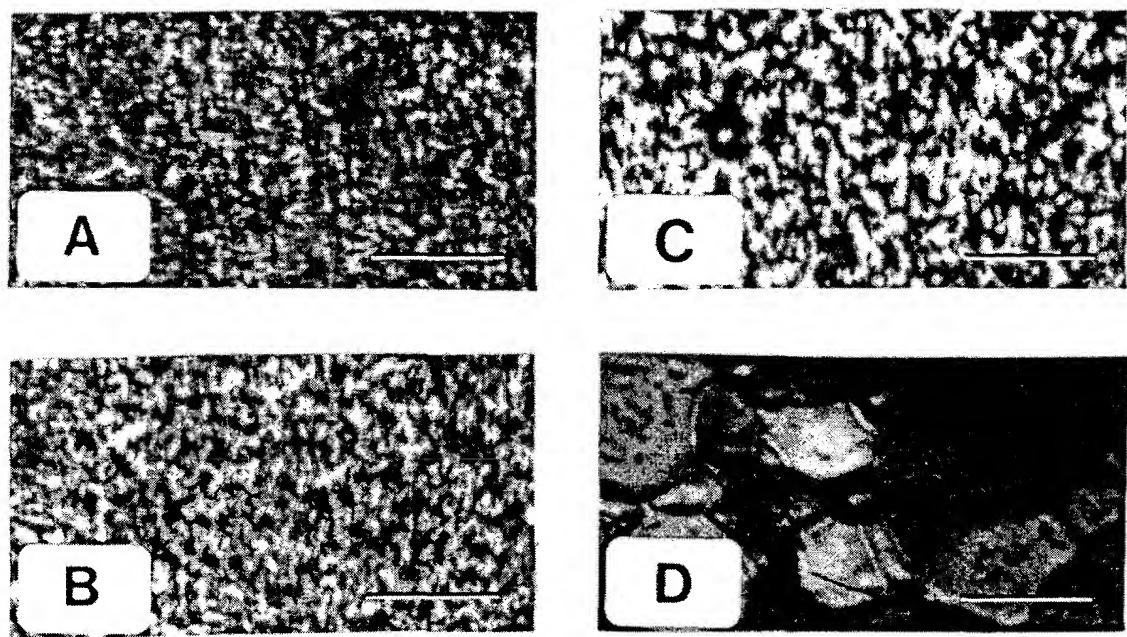


FIG. 8.7

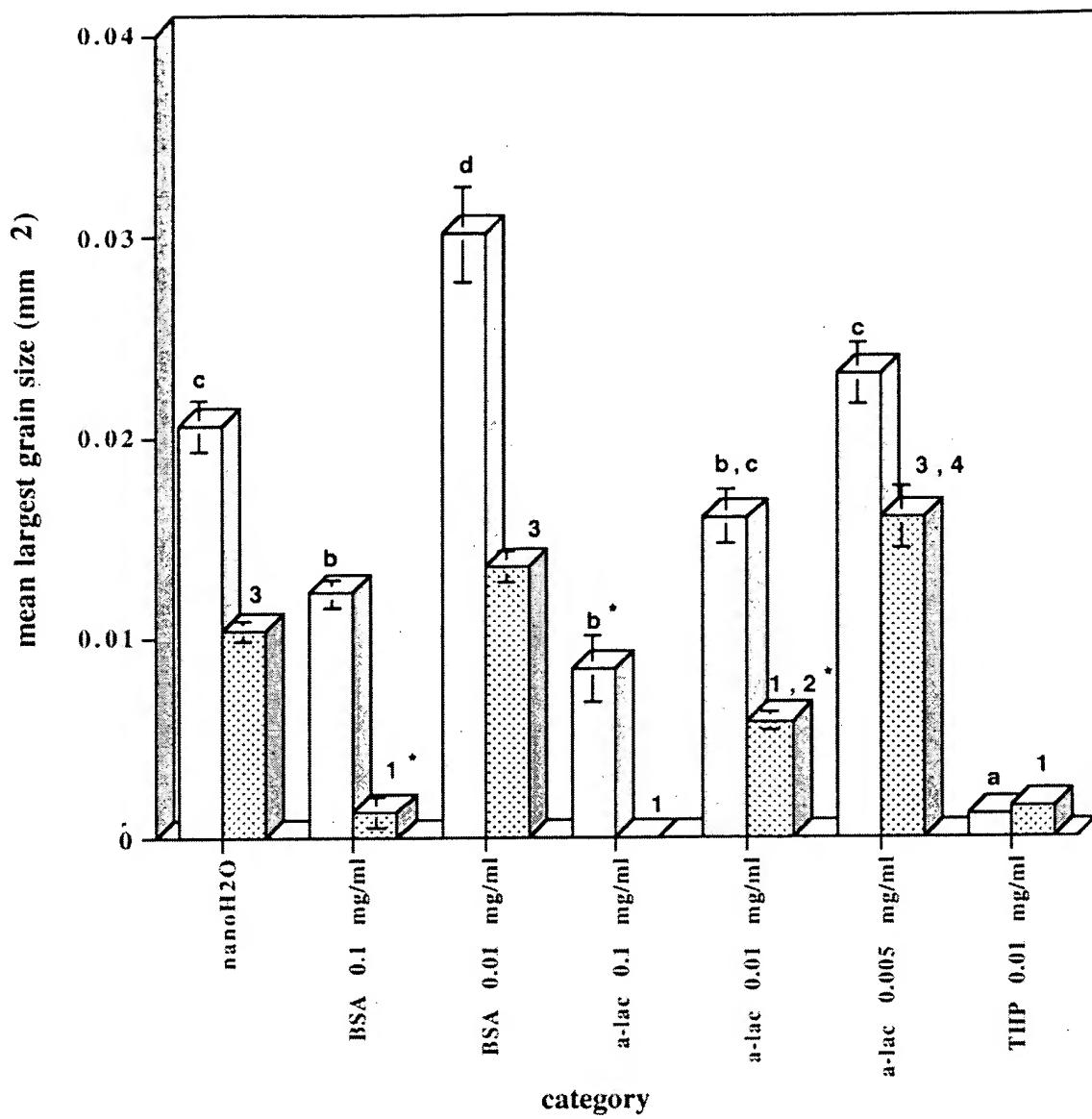


FIG. 8.8

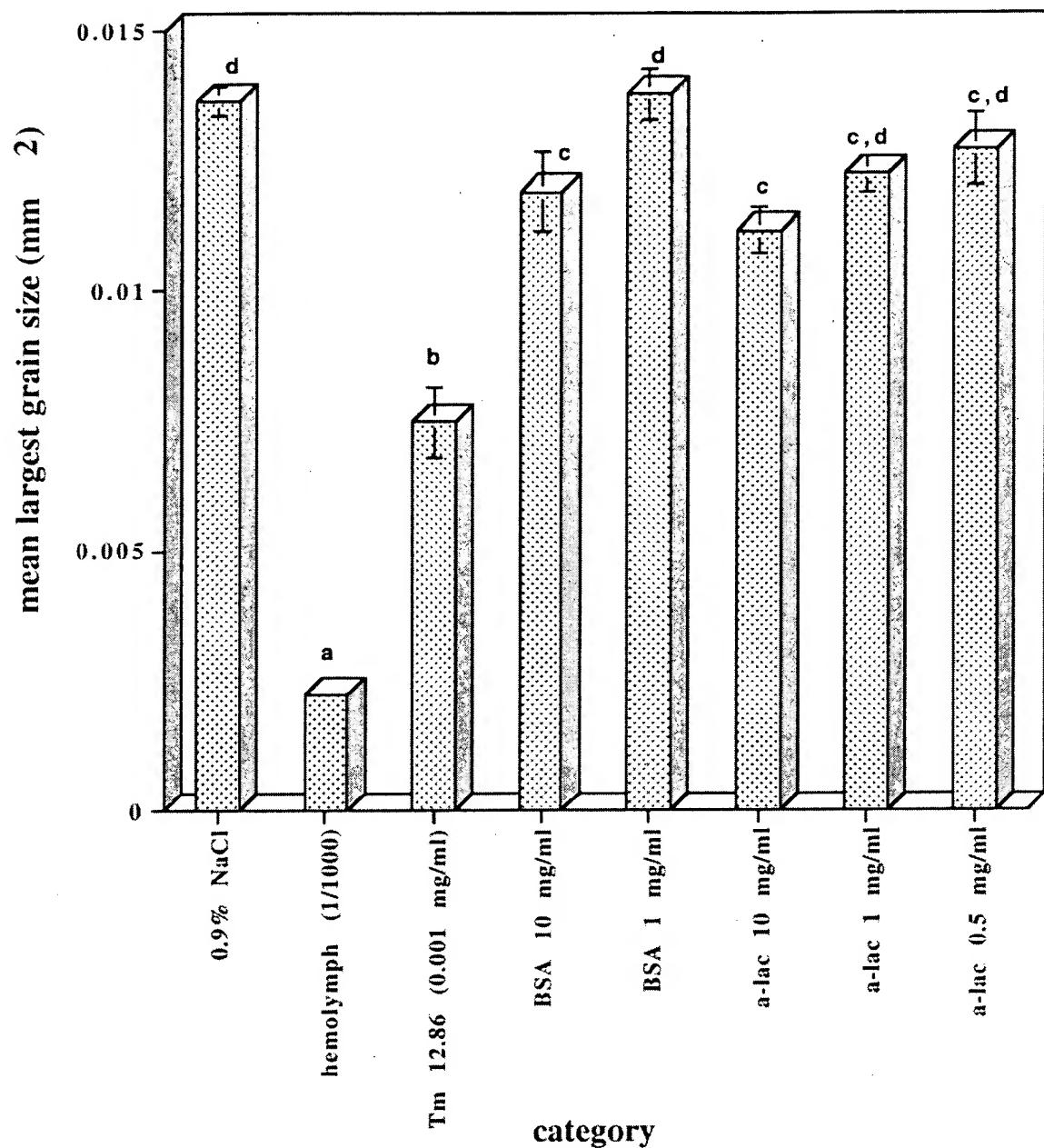


FIG. 8.9

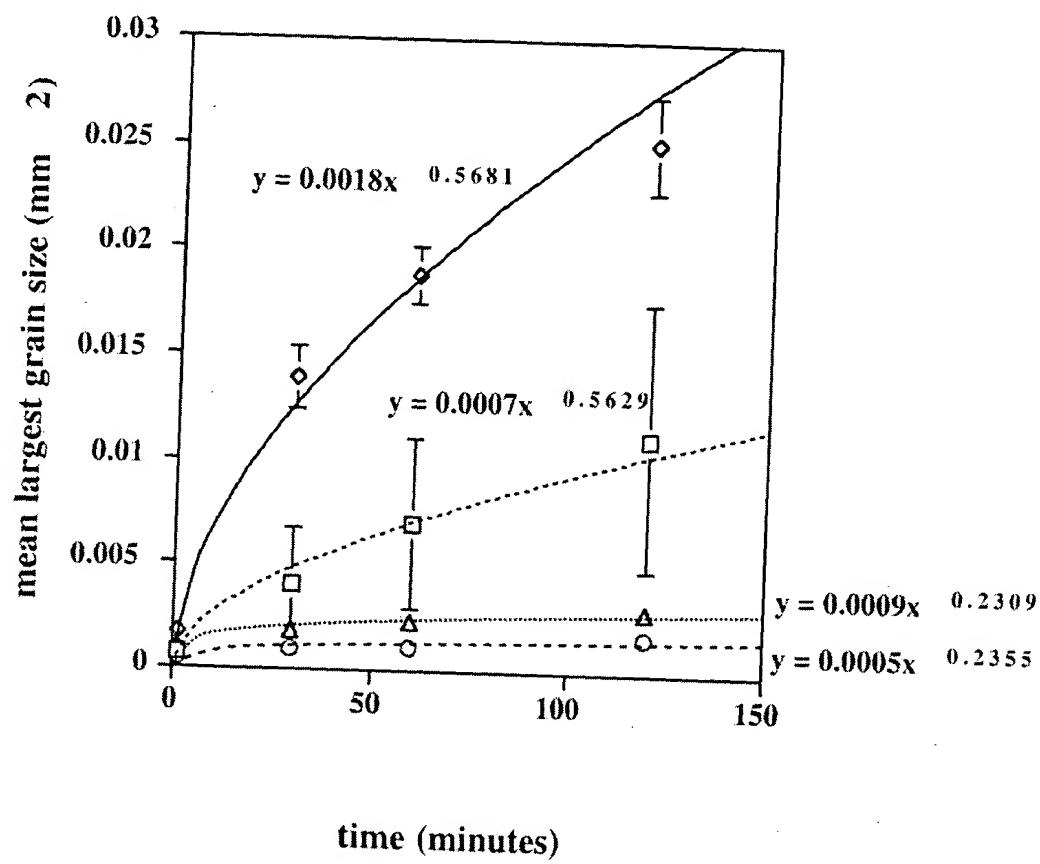
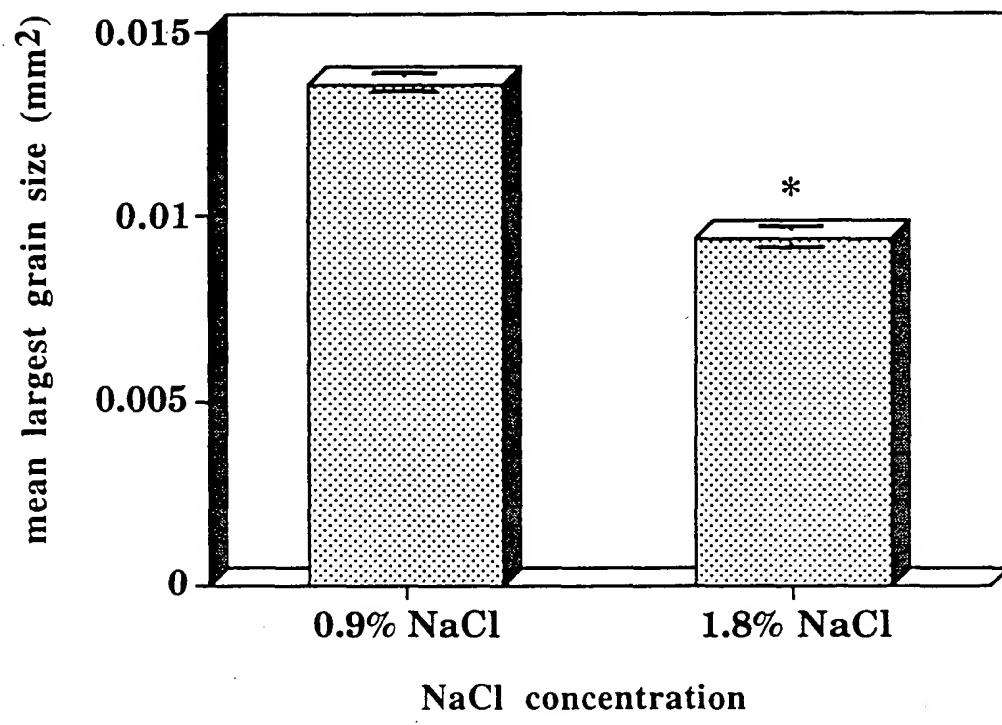


FIG. 8.10



**FIG. 8.11**

FIGURE 8.12

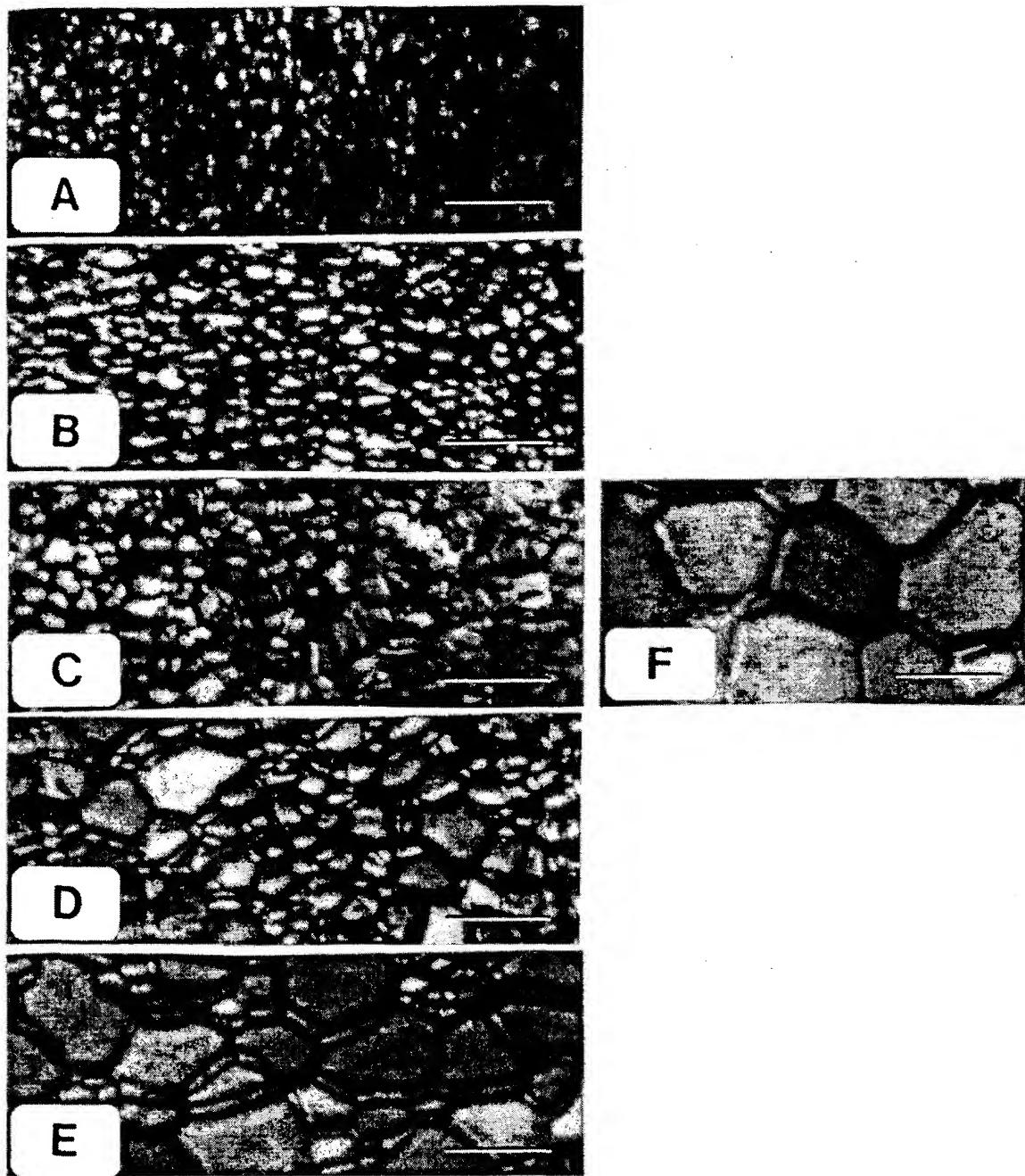


FIG. 8.12

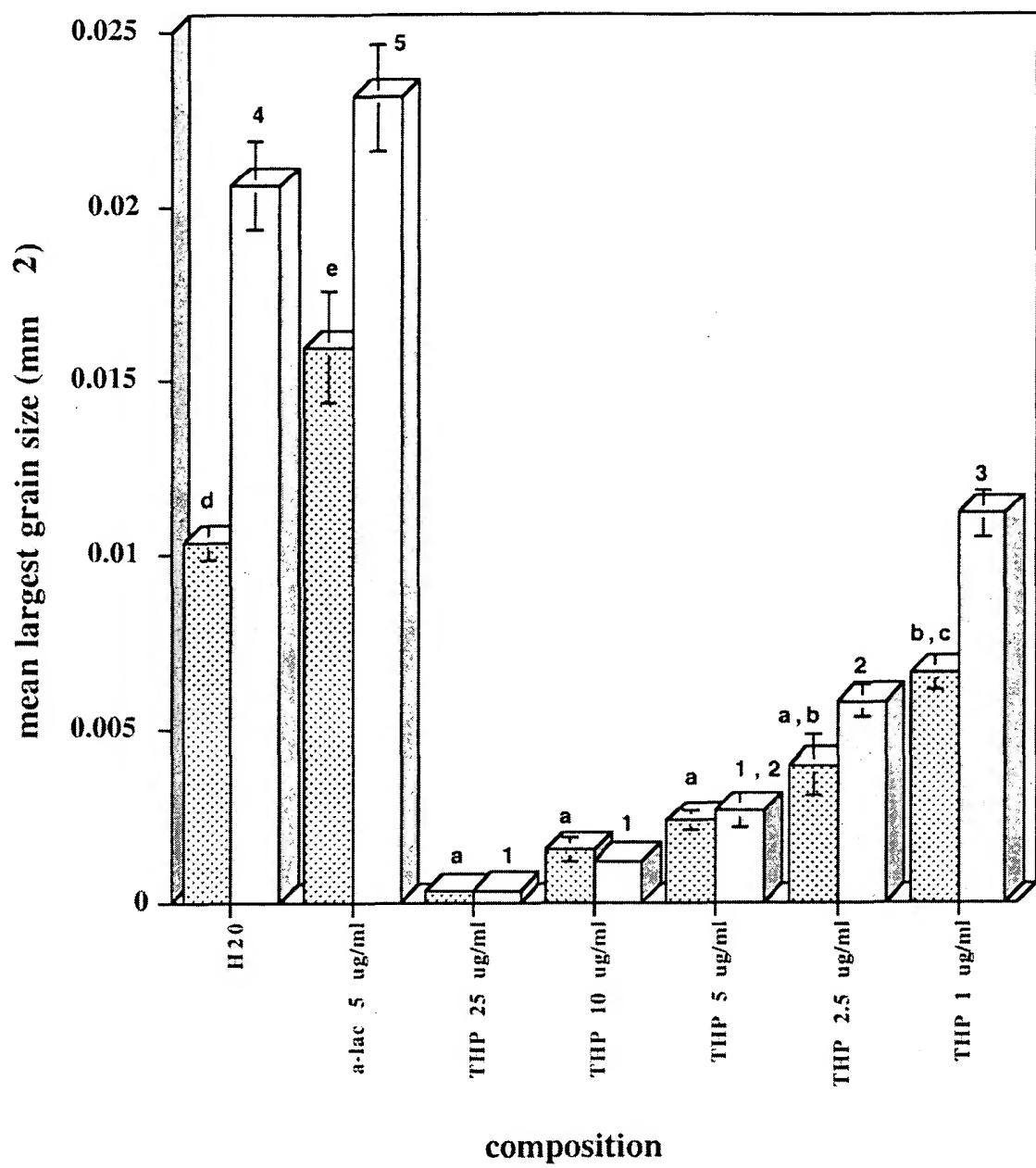


FIG. 8.13

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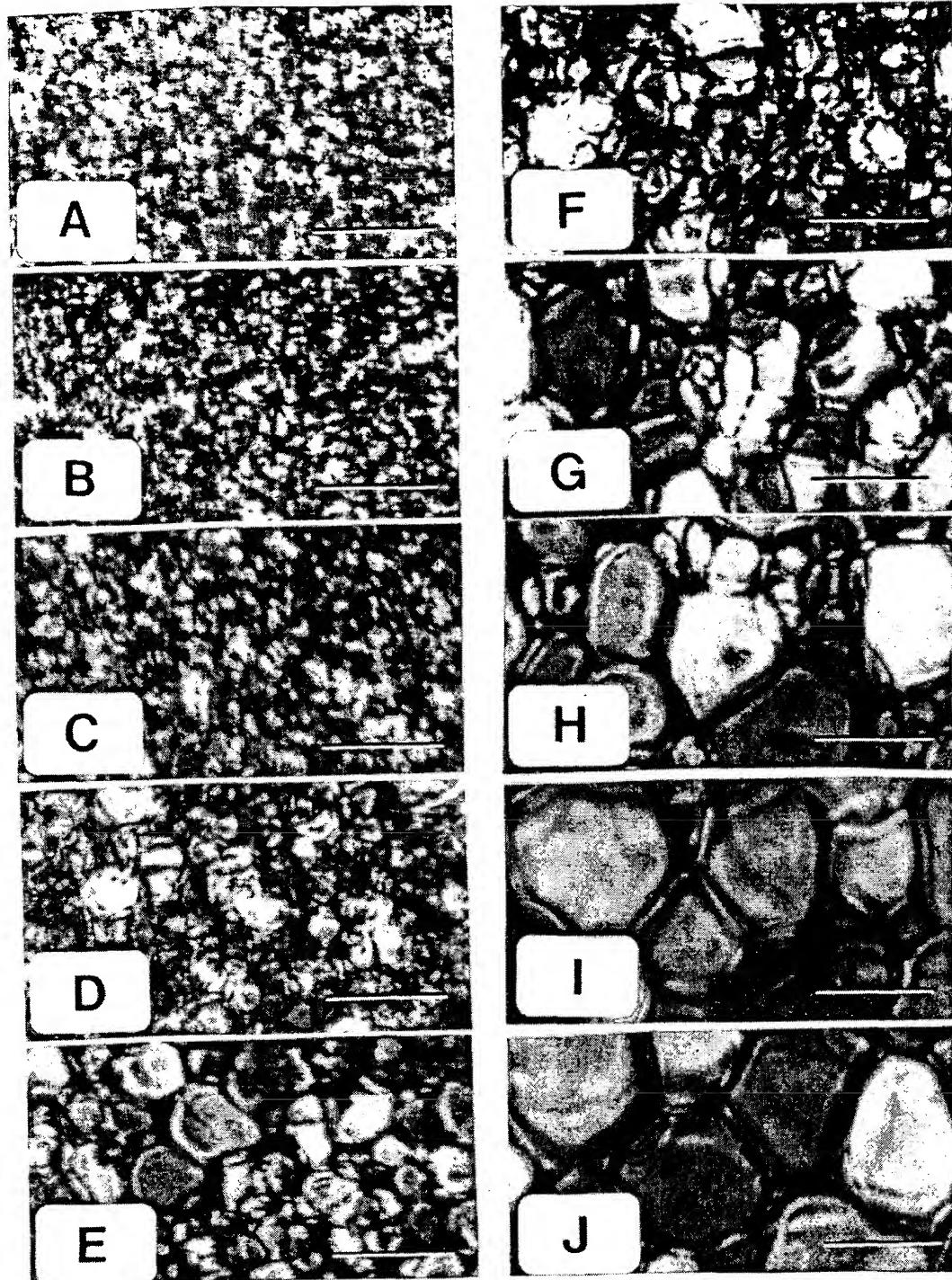


FIG. 8.14

0.02  
0.015  
0.01  
0.005  
0

mean largest grain size ( $\text{mm}^2$ )

■ -60 °C  
□ -20 °C

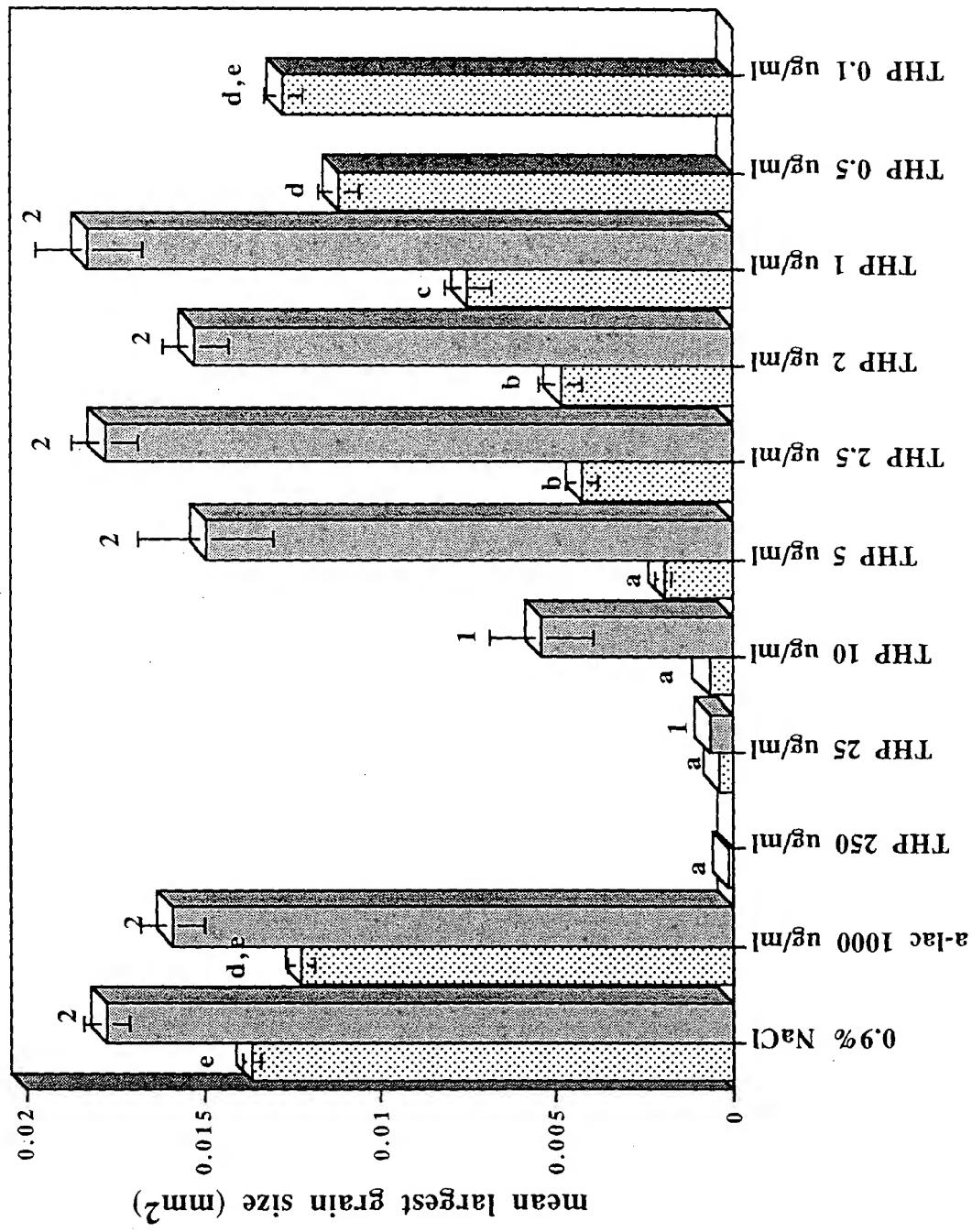


FIG. 8.15

11 0 0 0 0 0 0 0 0 0 0

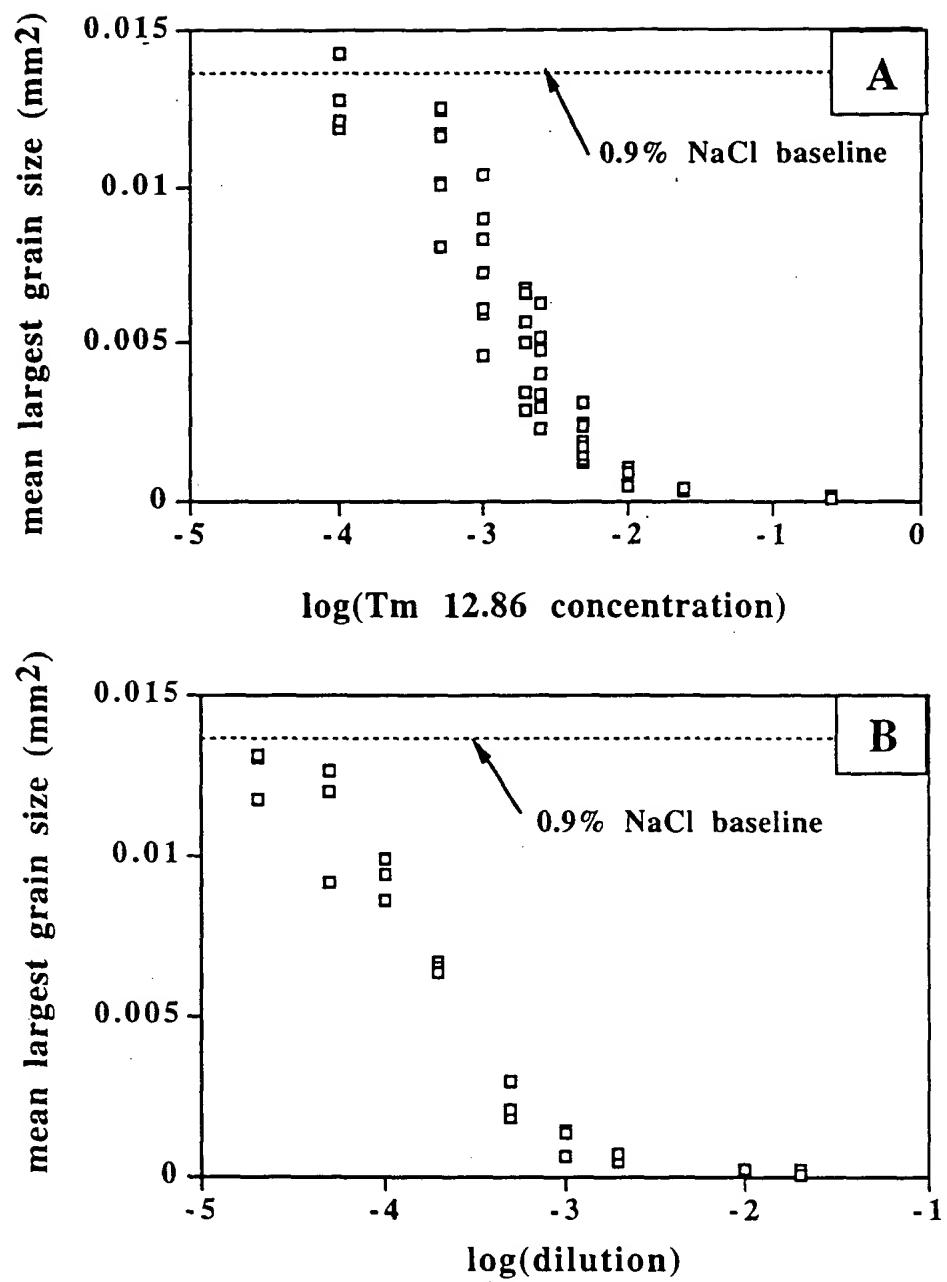


FIG. 8.16

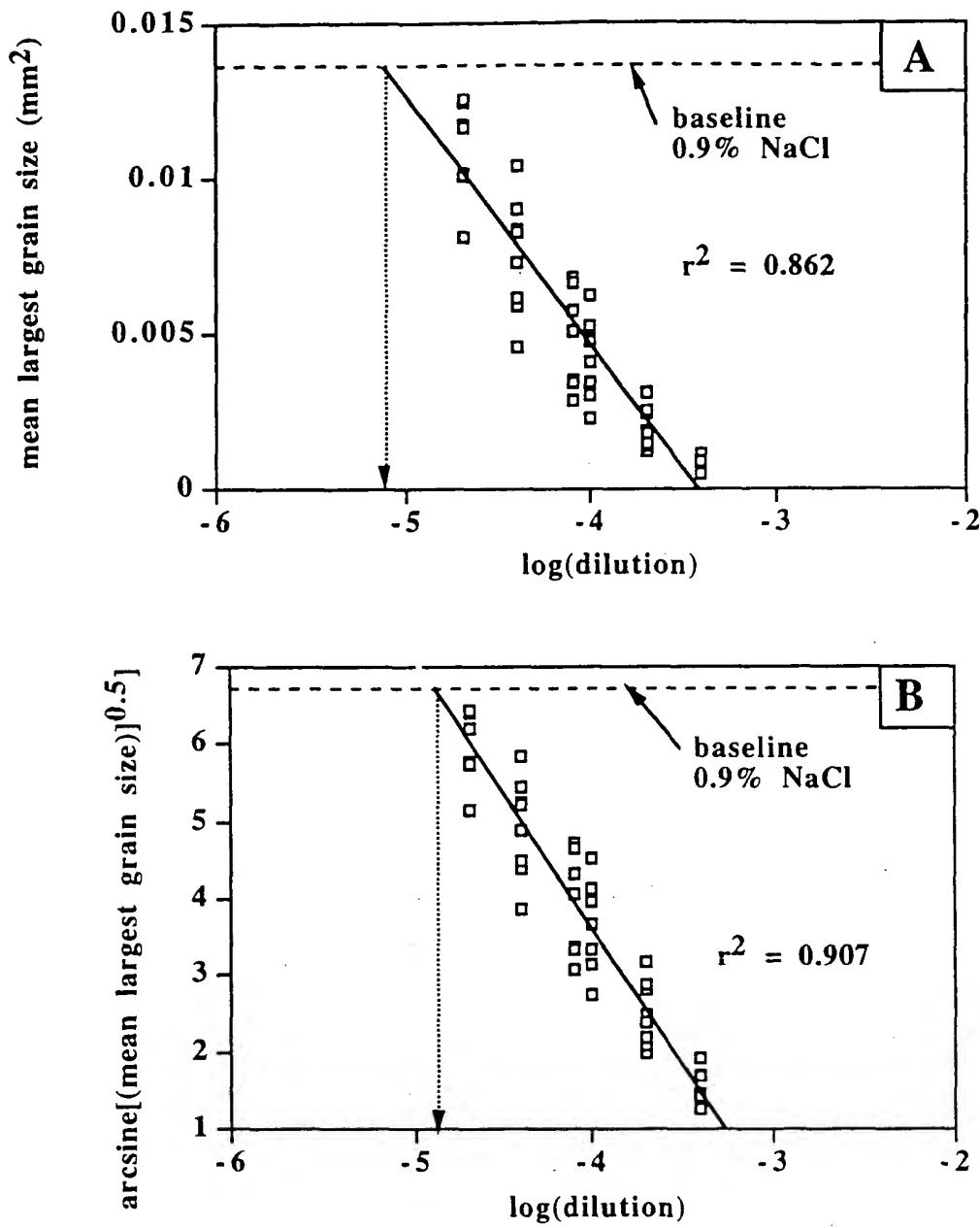


FIG. 8.17

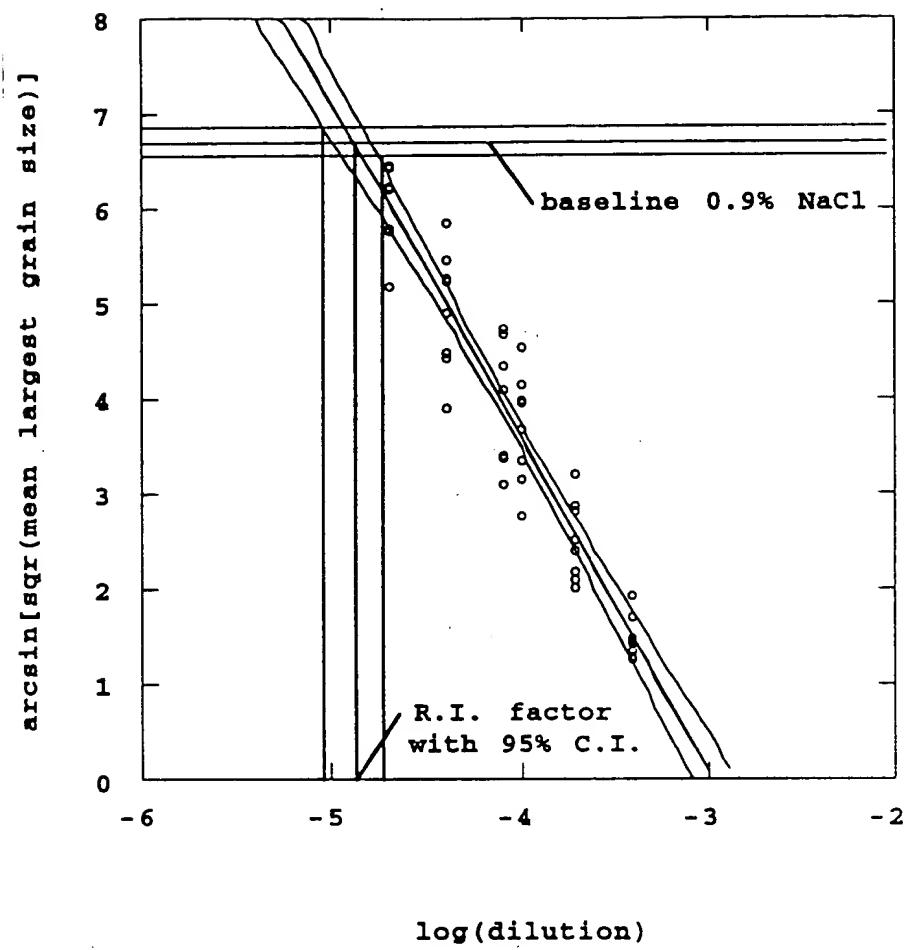


FIG. 8.18

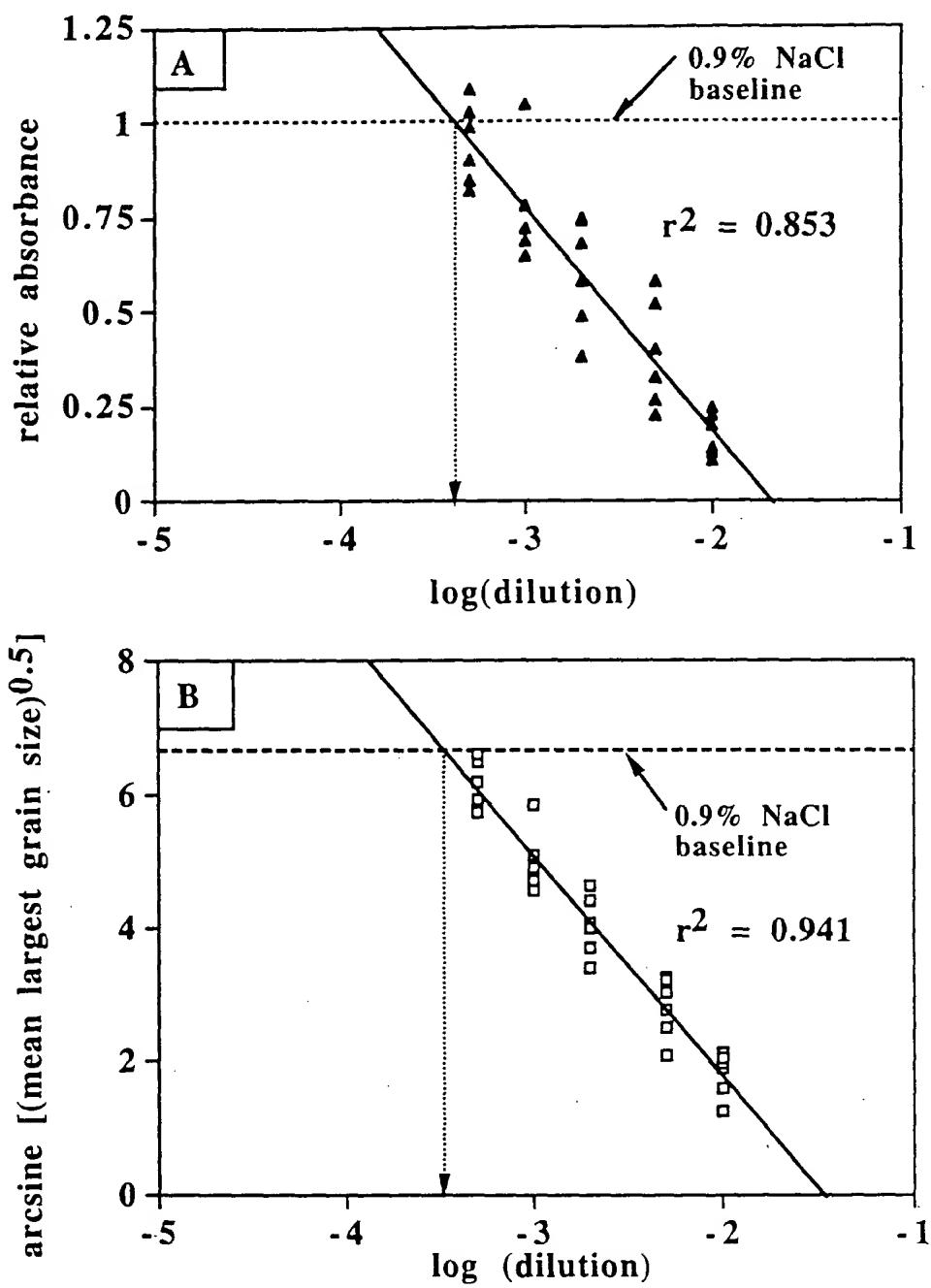


FIG. 8.19

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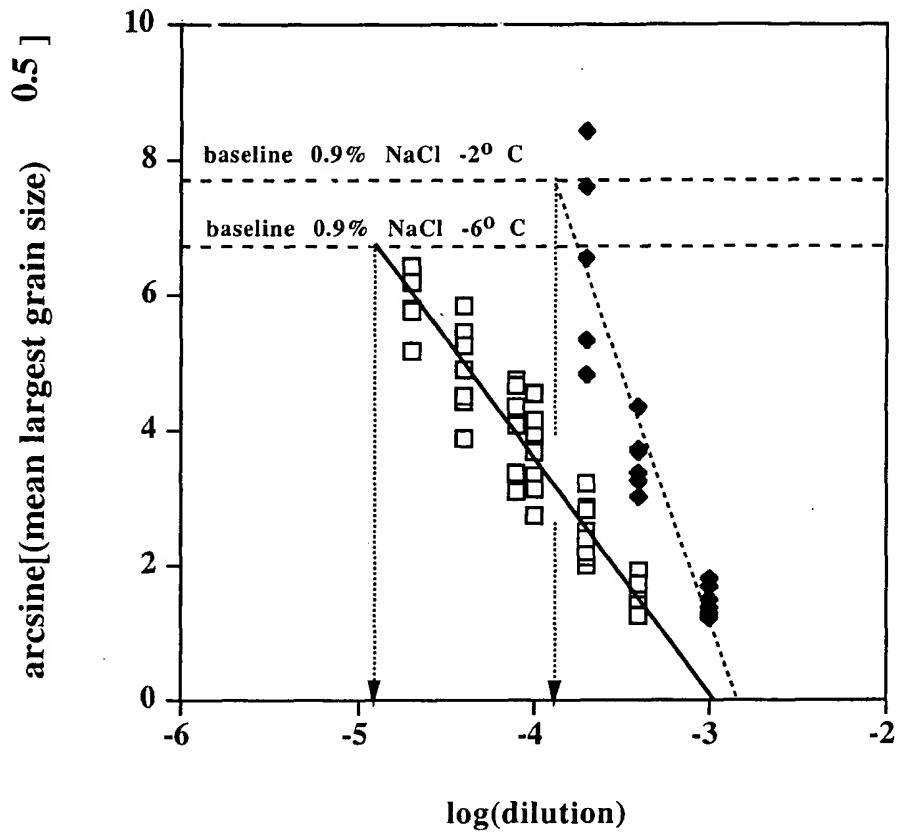


FIG. 8.20

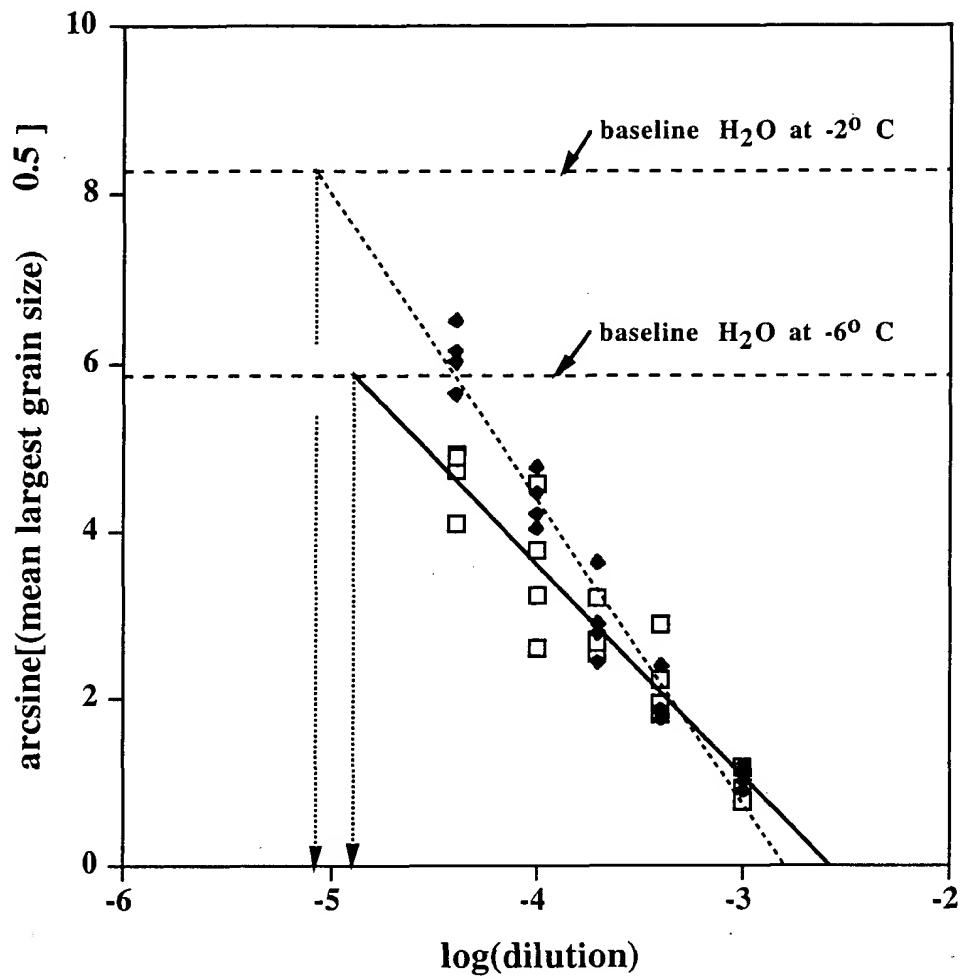


FIG. 8.21

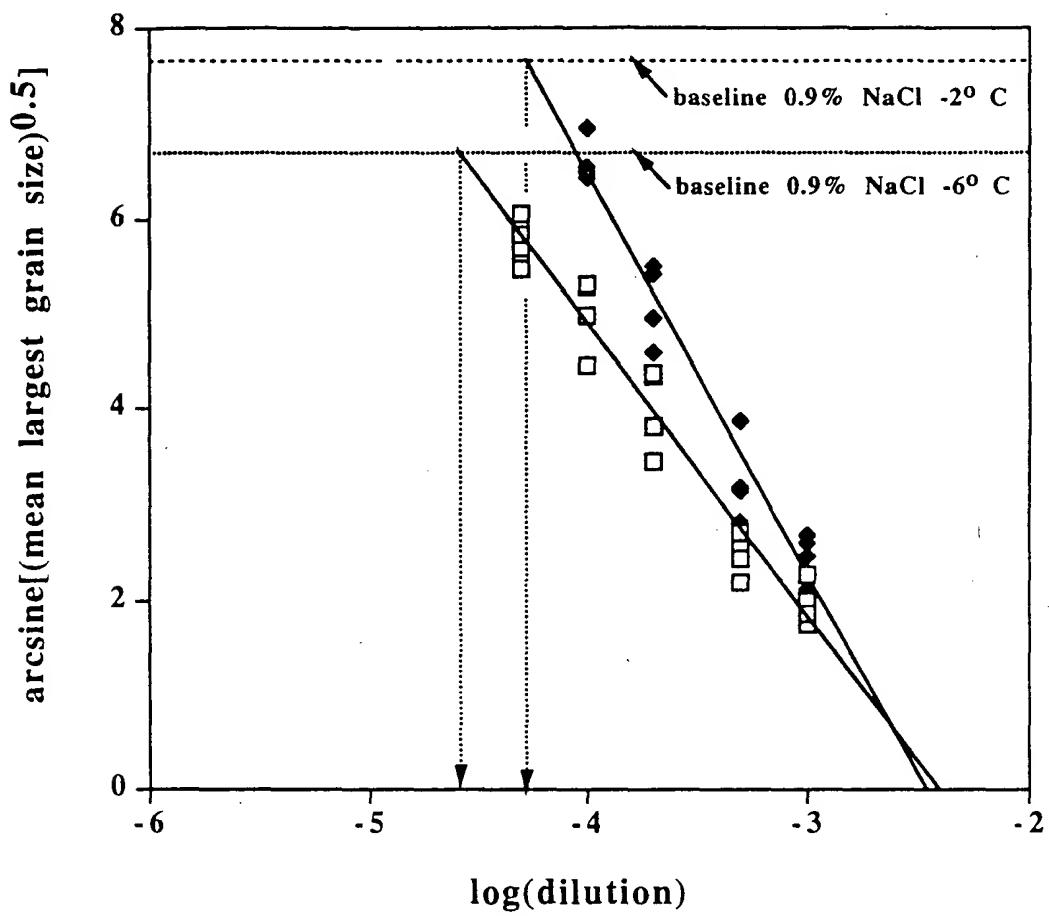


FIG. 8.22

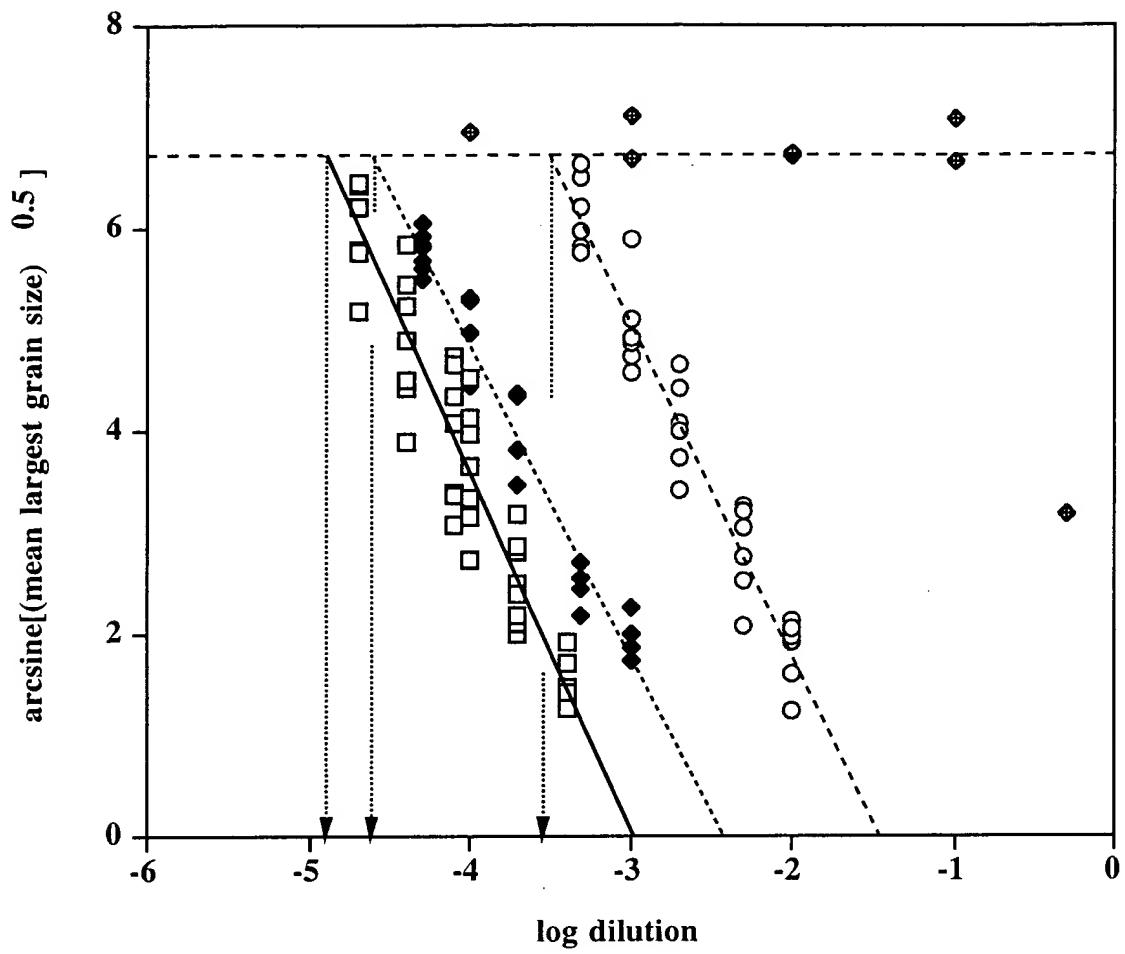
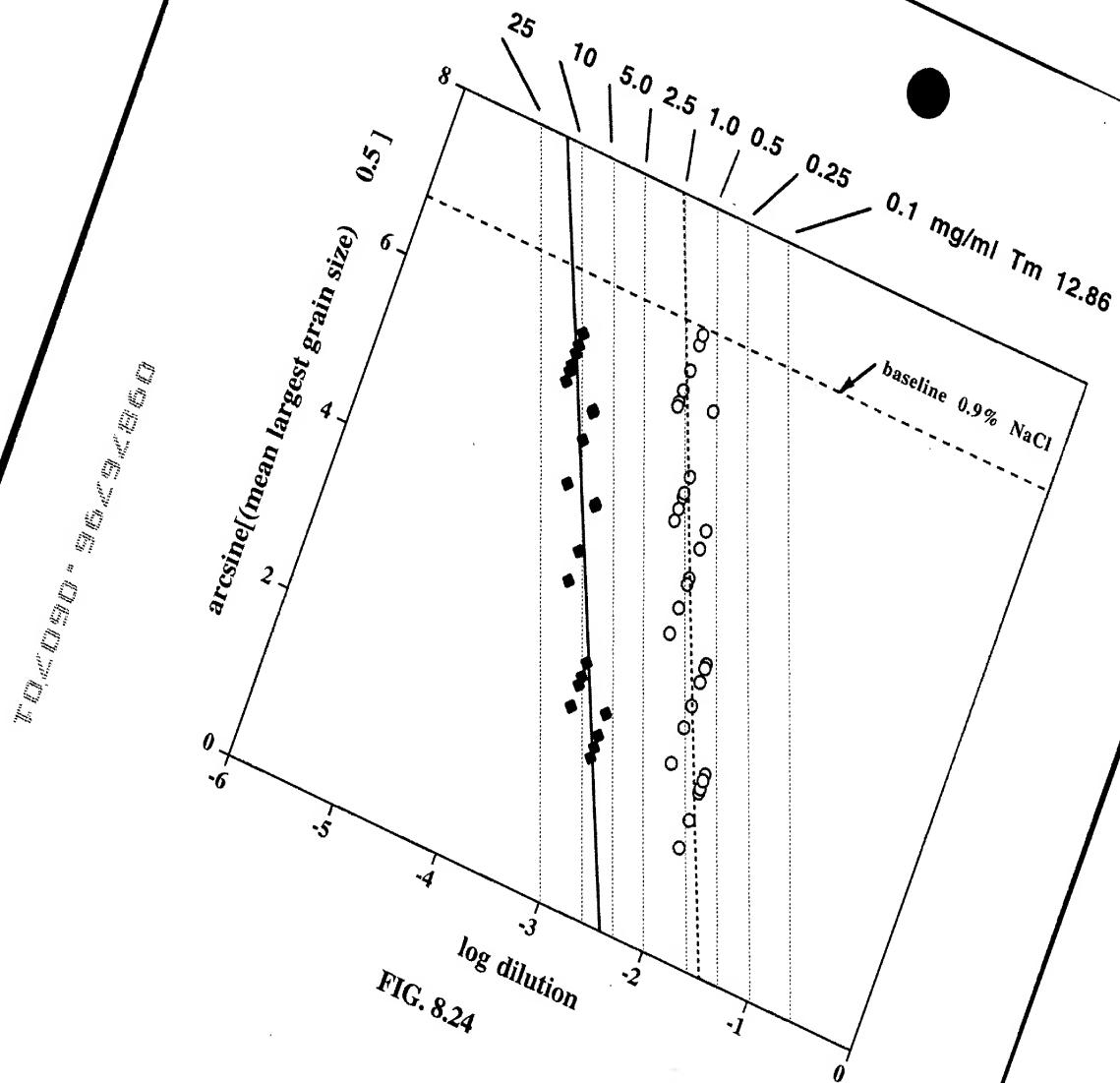


FIG. 8.23



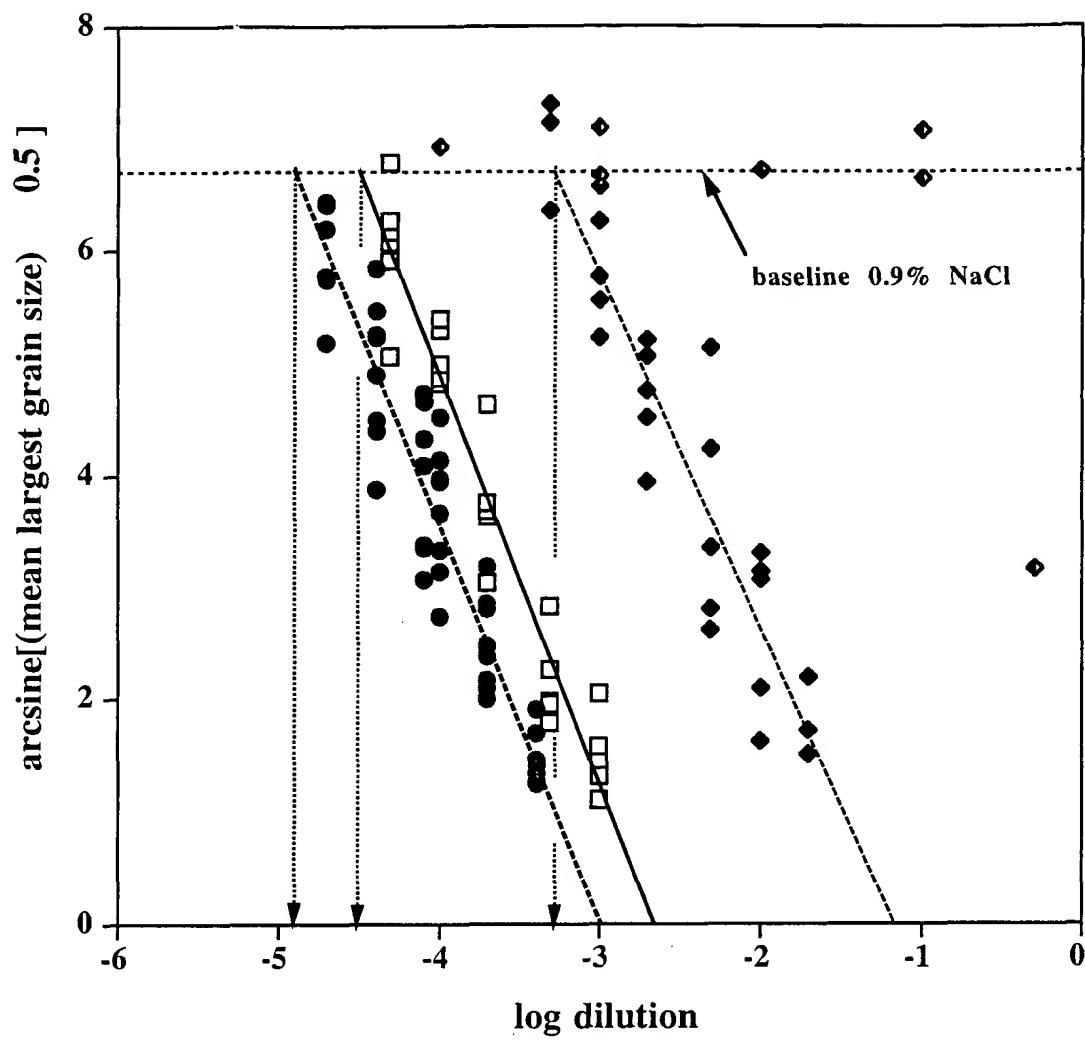


FIG. 8.25

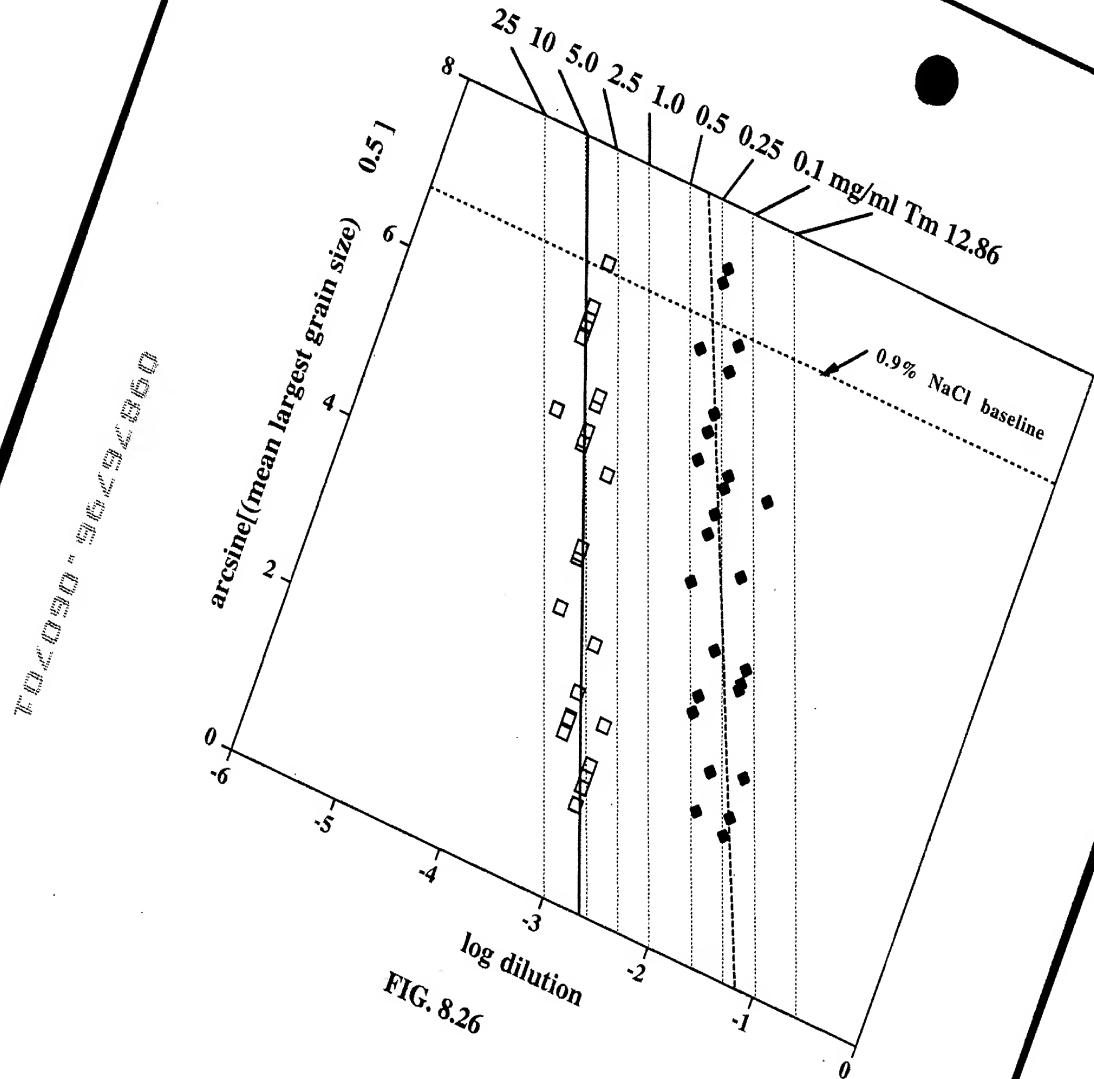


FIG. 8.26

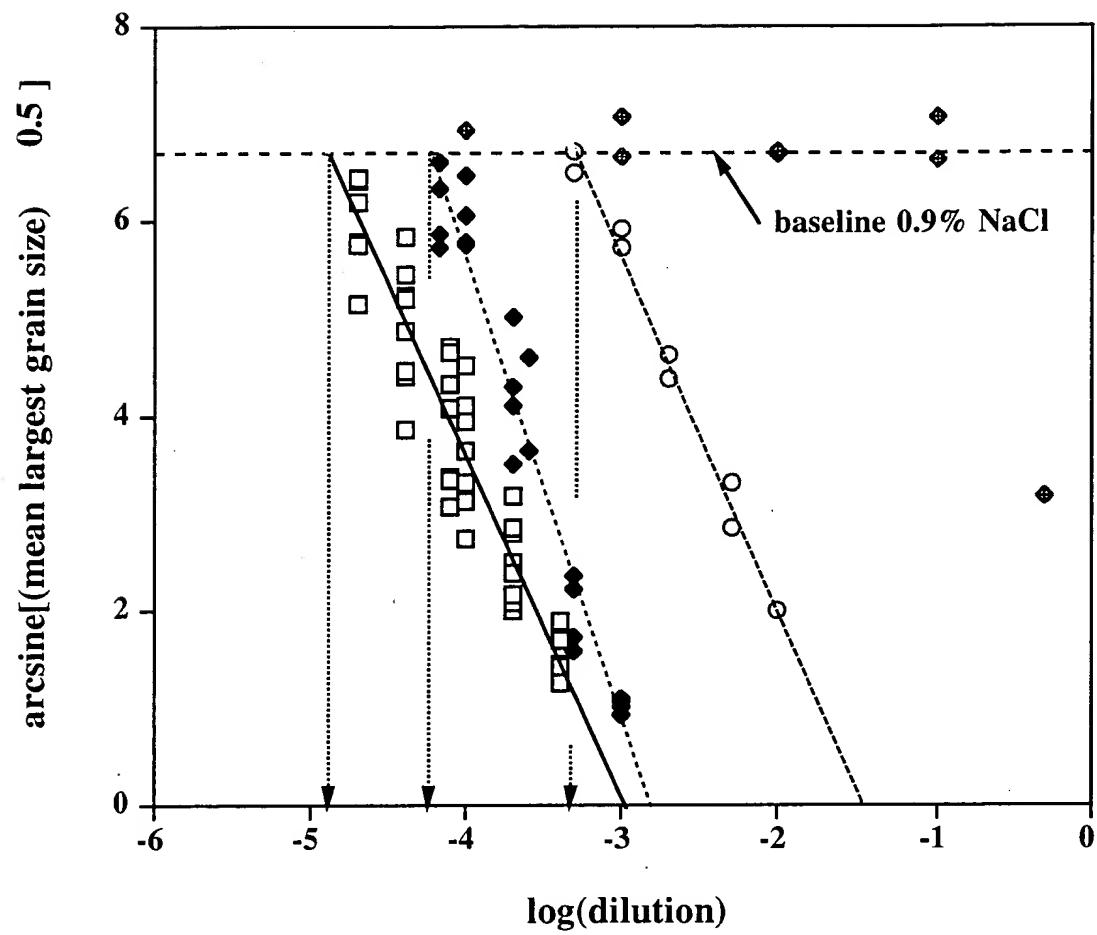


FIG. 8.27

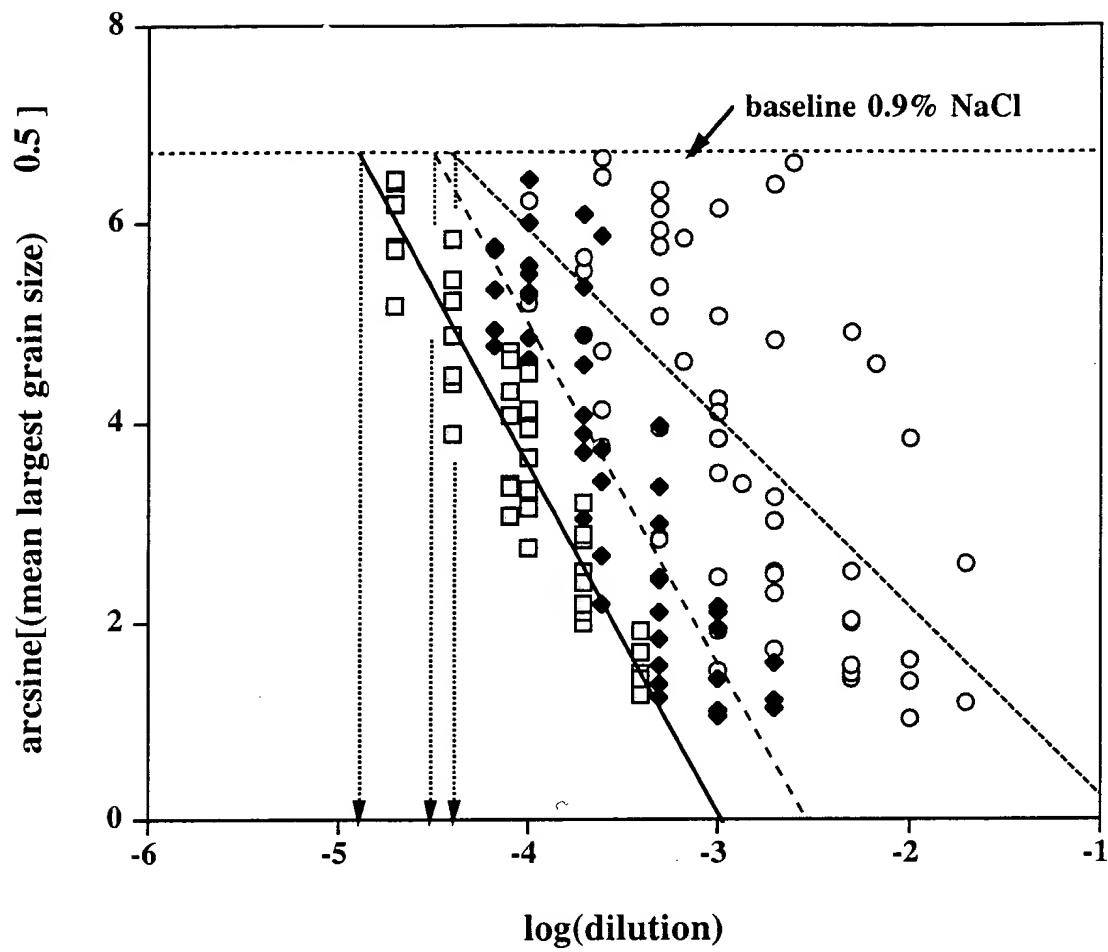


FIG. 8.28

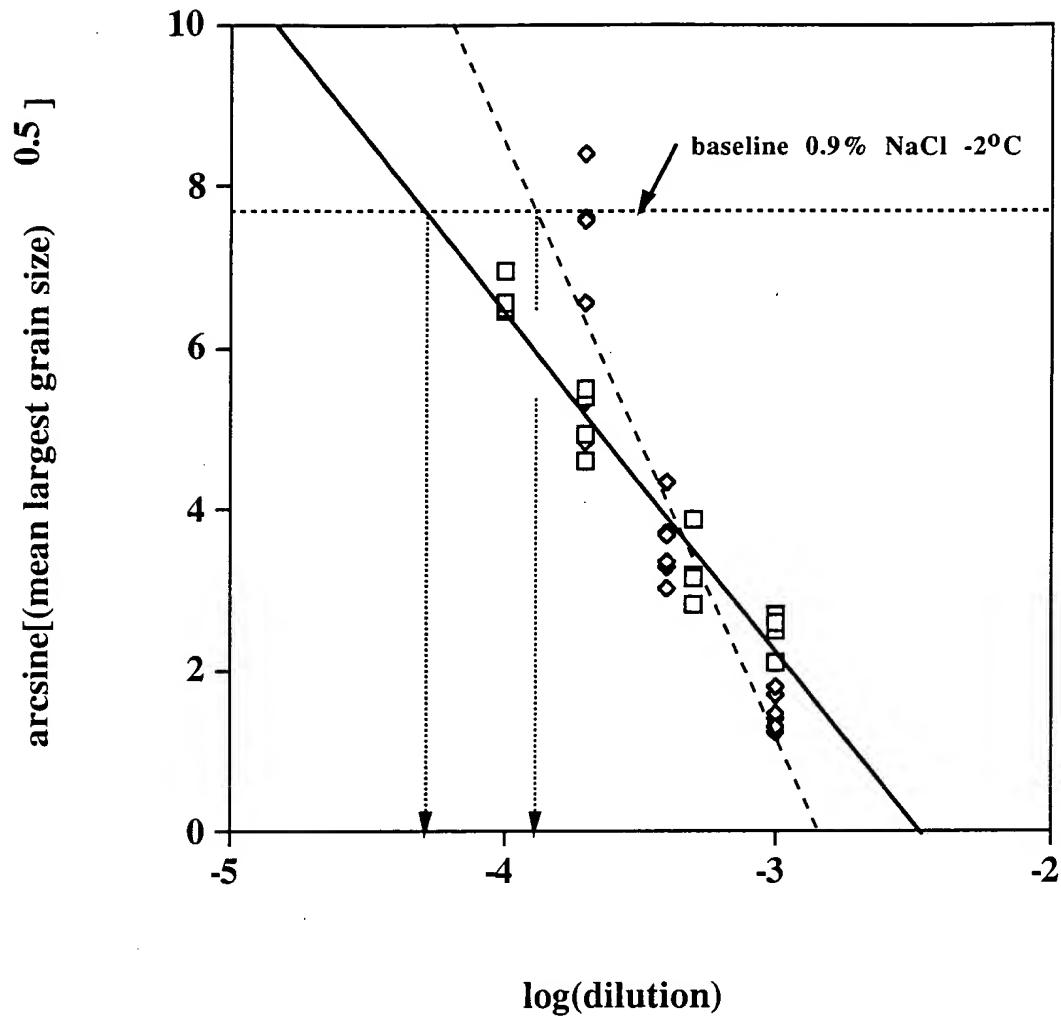


FIG. 8.29

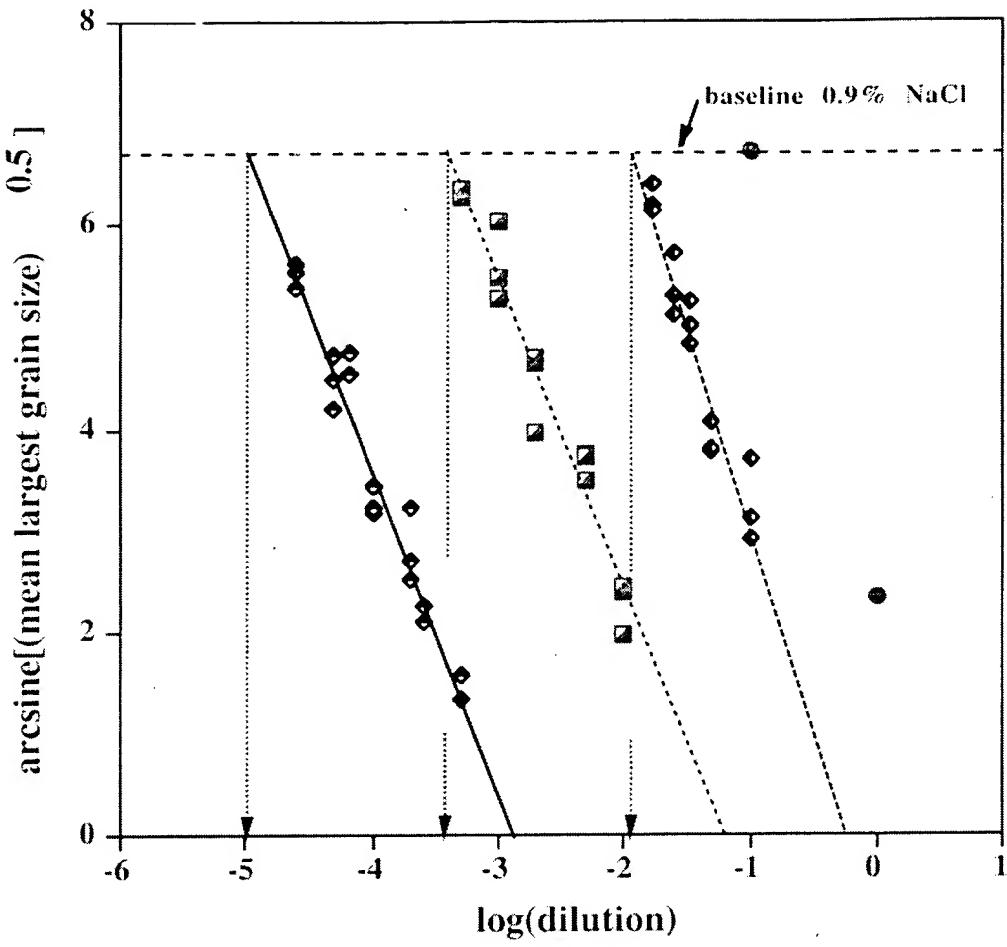


FIG. 8.30

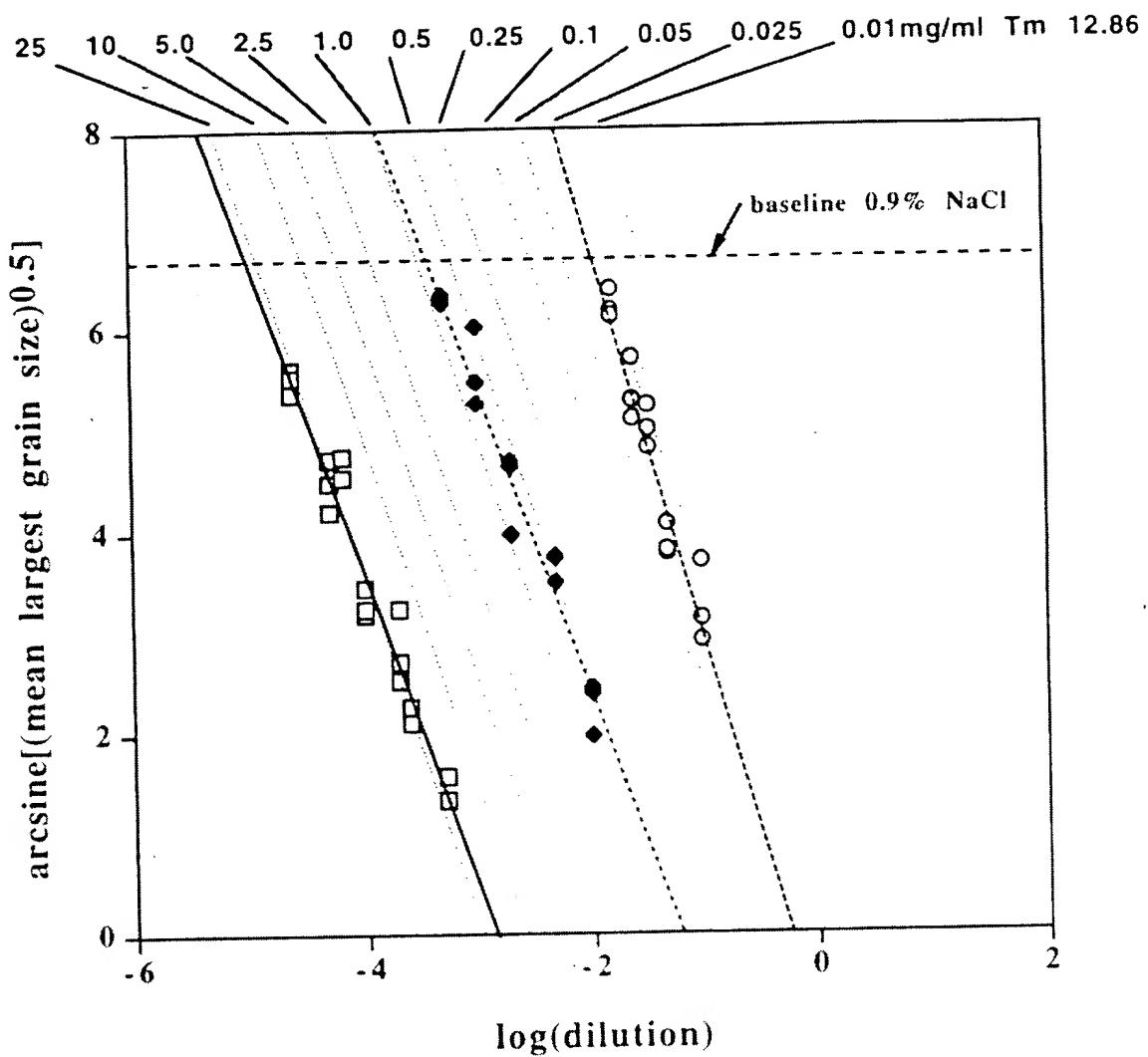


FIG. 8.31

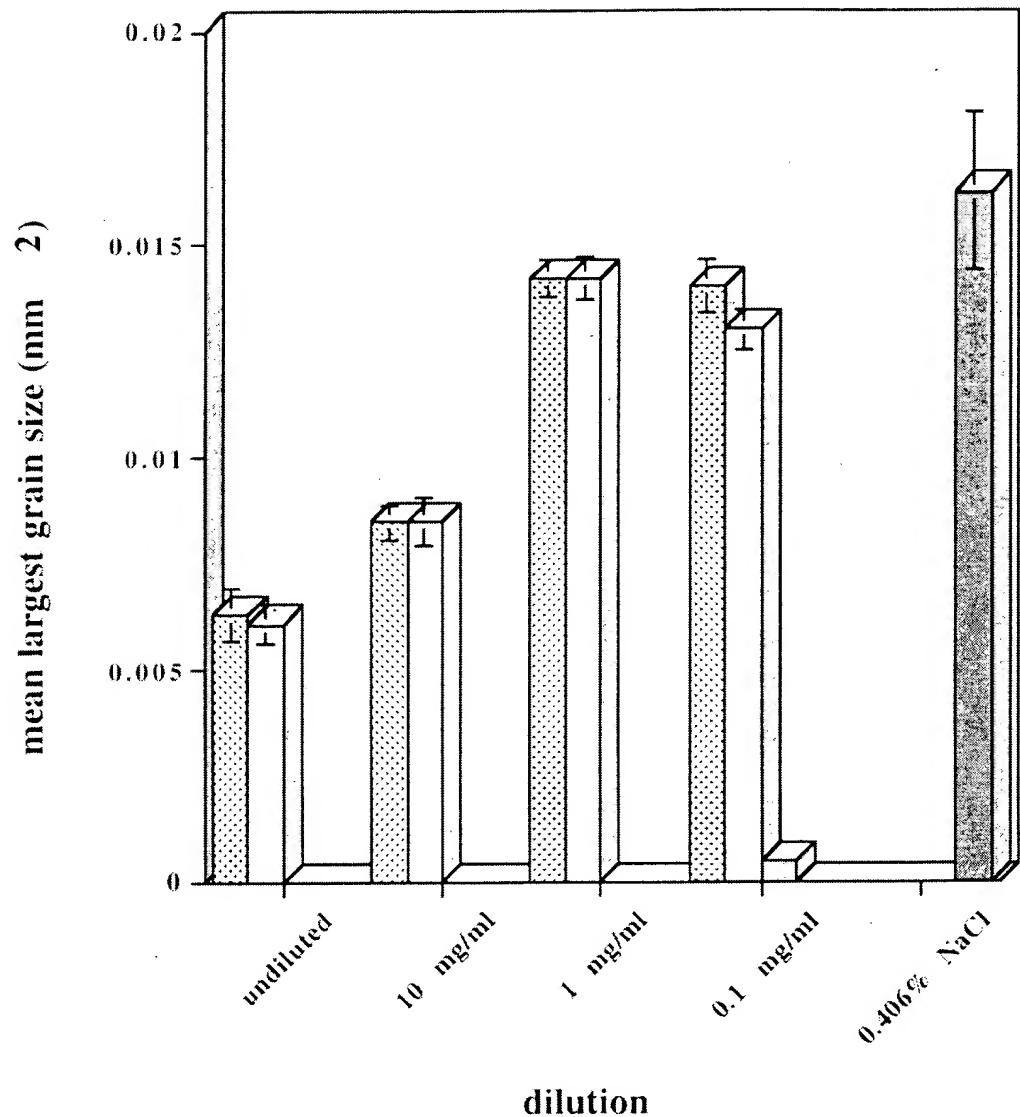


FIG. 8.32

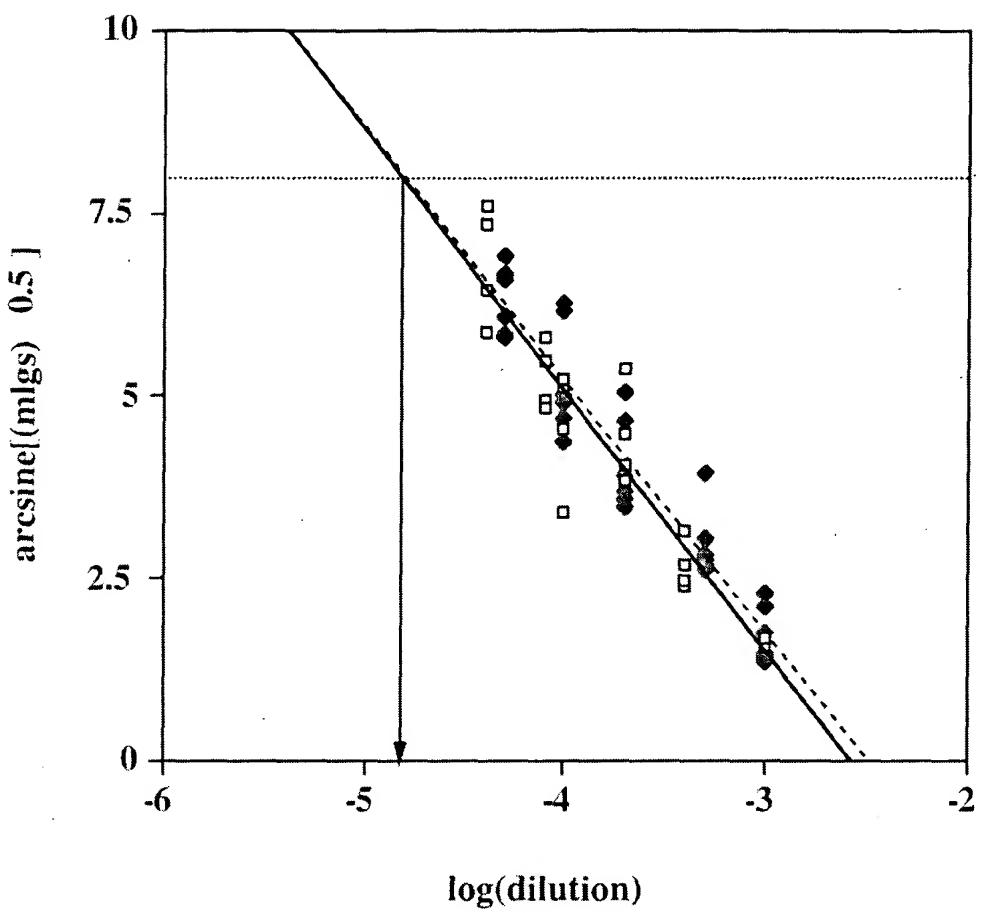


FIG. 8.33

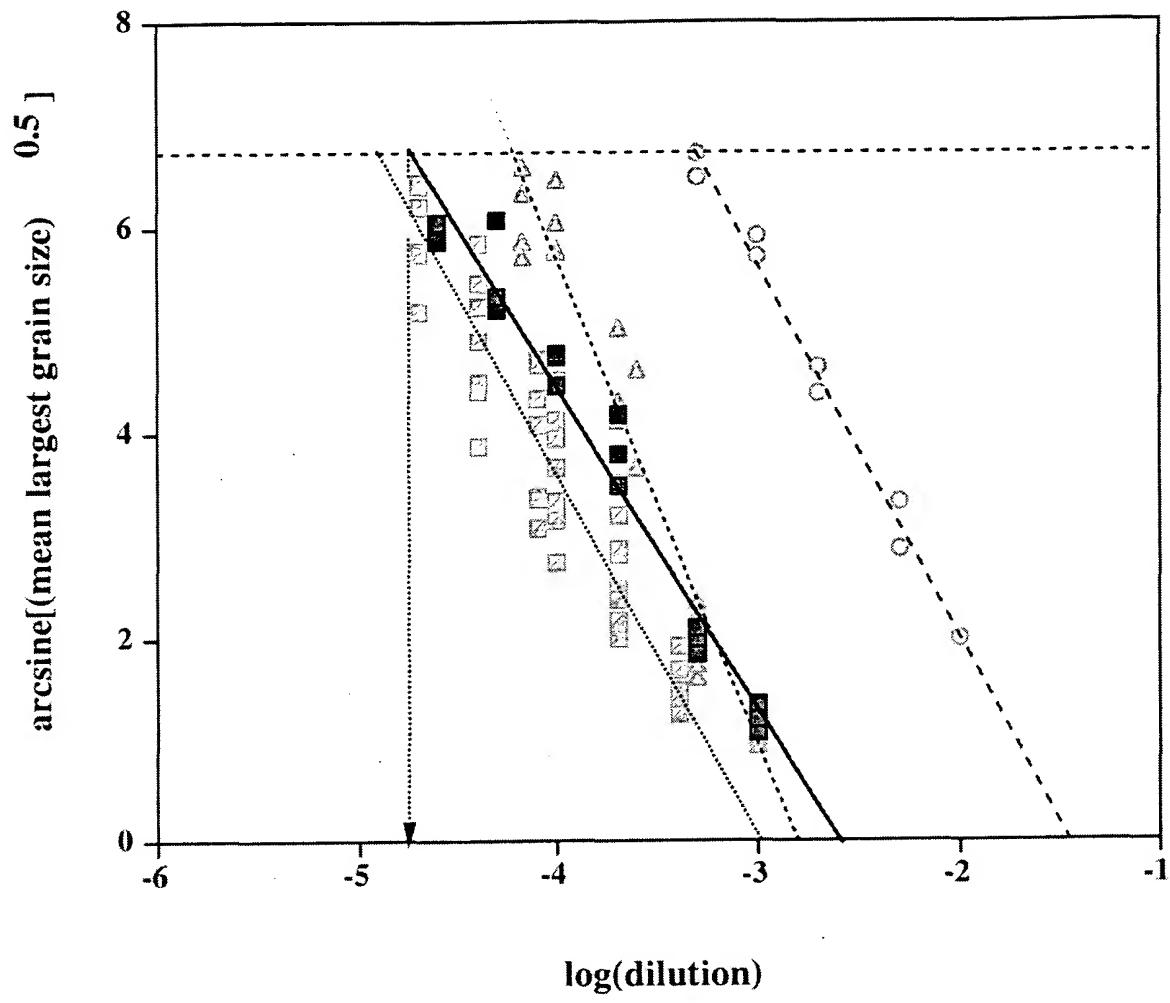


FIG. 8.34

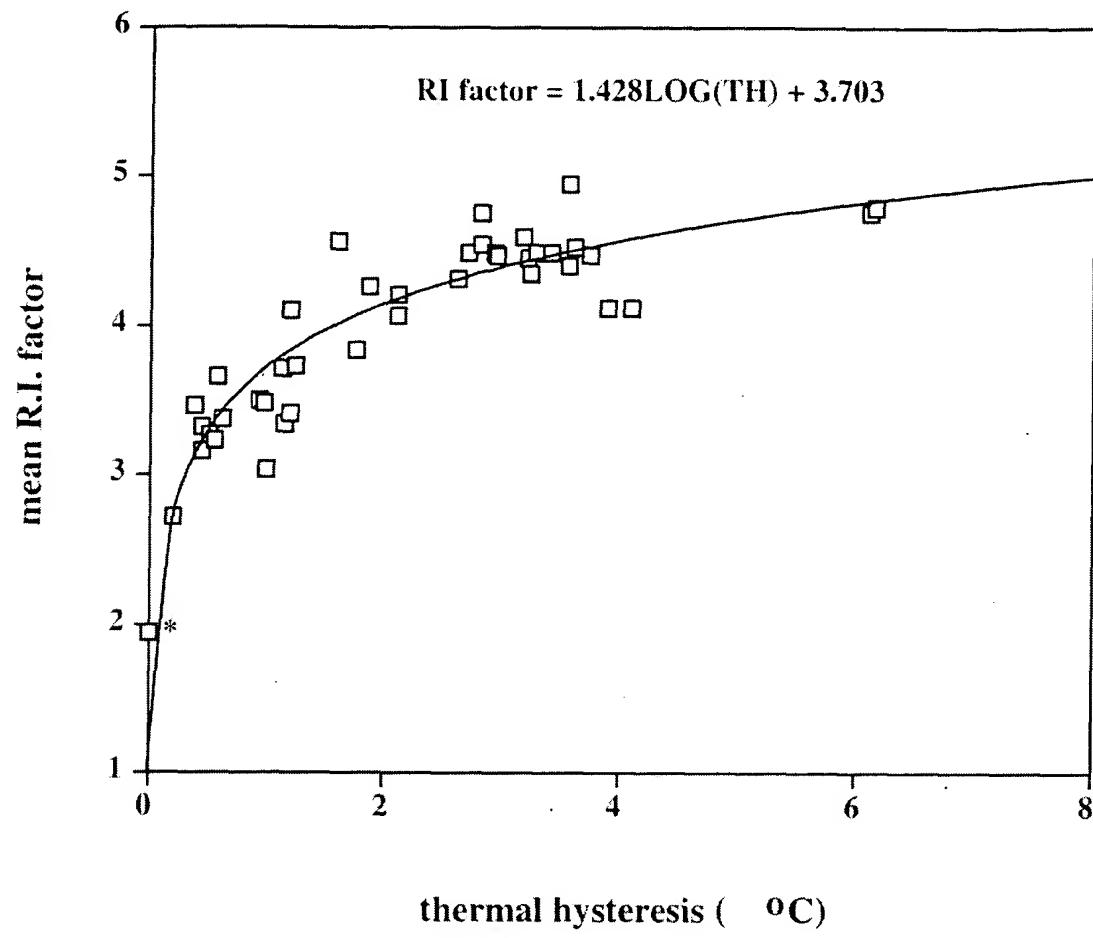


FIG. 8.35

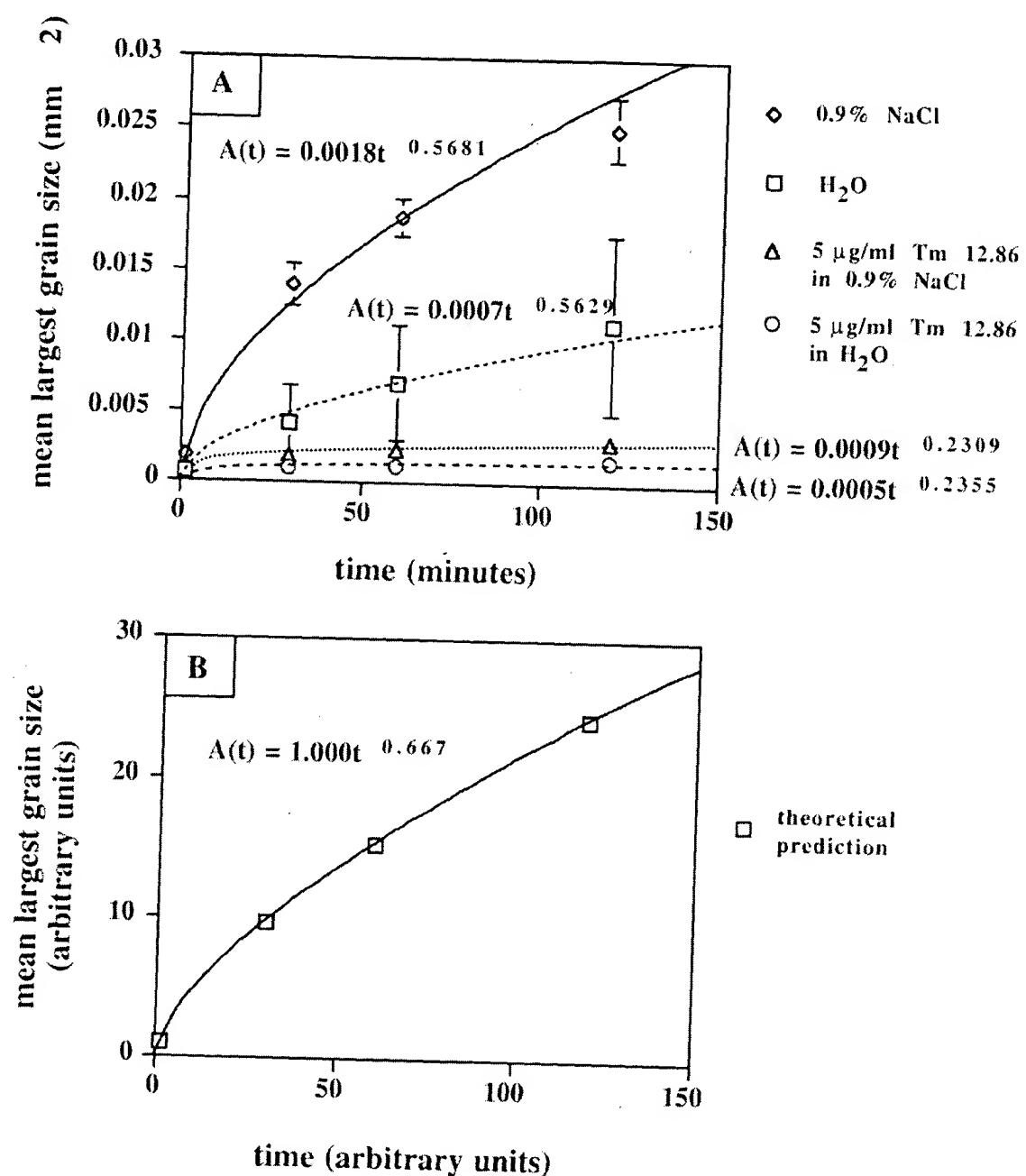


FIG. 8.36

Fig. 8.37. Effect of time on mean largest grain size.

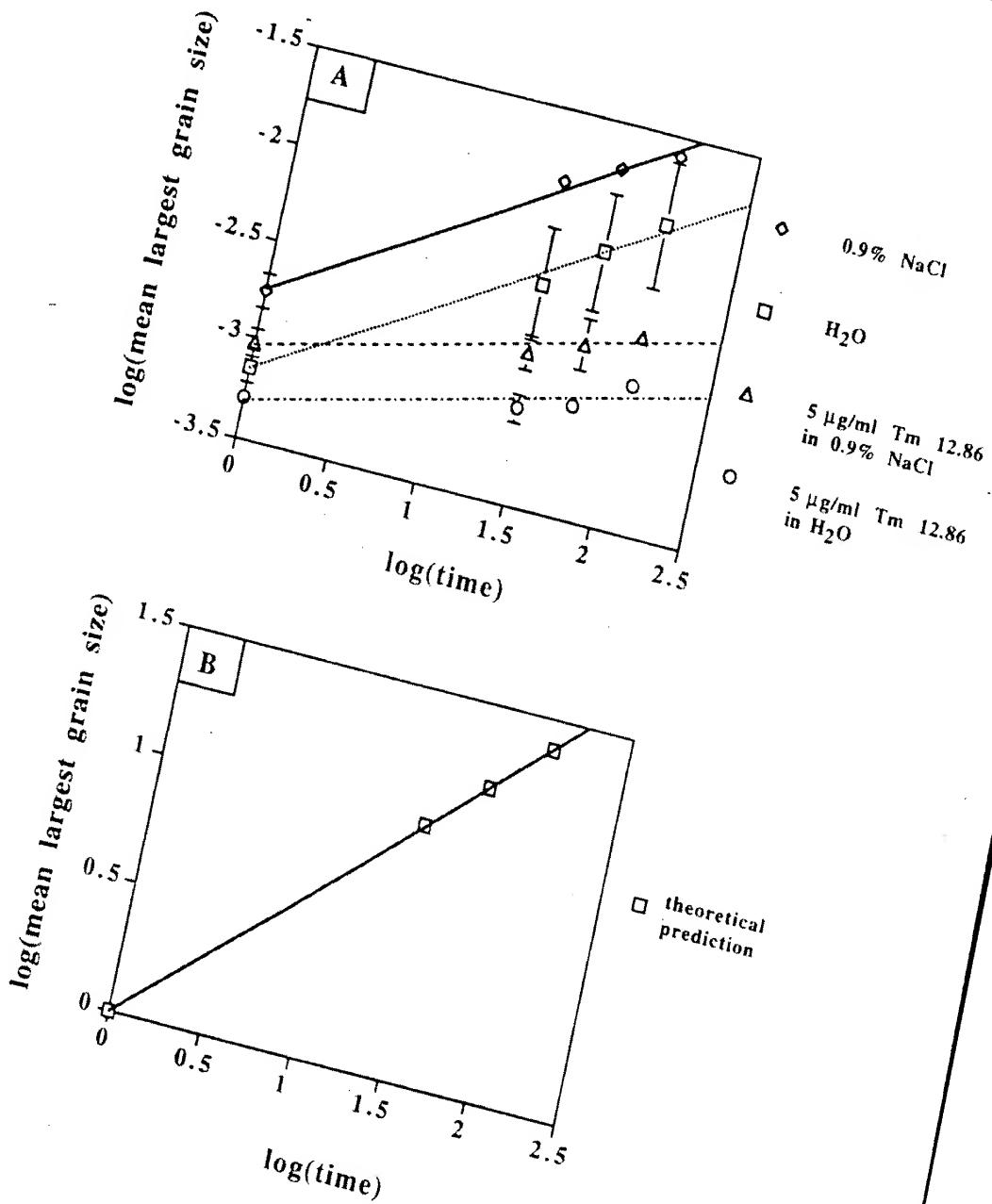
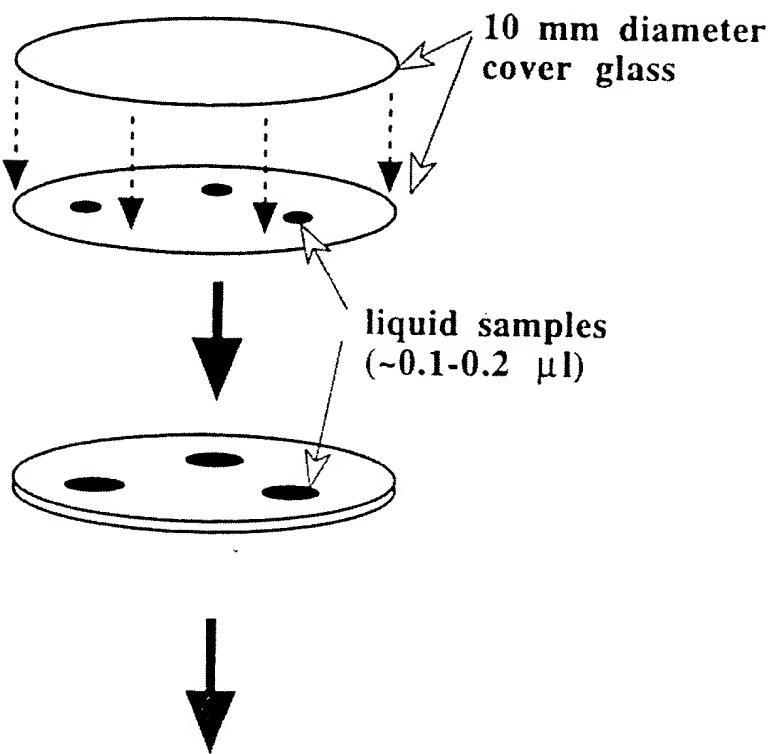


FIG. 8.37

## "Sandwich" method of R.I. assessment

1.



2.

3. FREEZE ON ~-80 C  
ALUMINUM PLATE (~10 MIN.)



4. PLACE ON COLD STAGE,  
ANNEAL AT -6 C UP TO  
12+ HOURS

FIG. 8.38

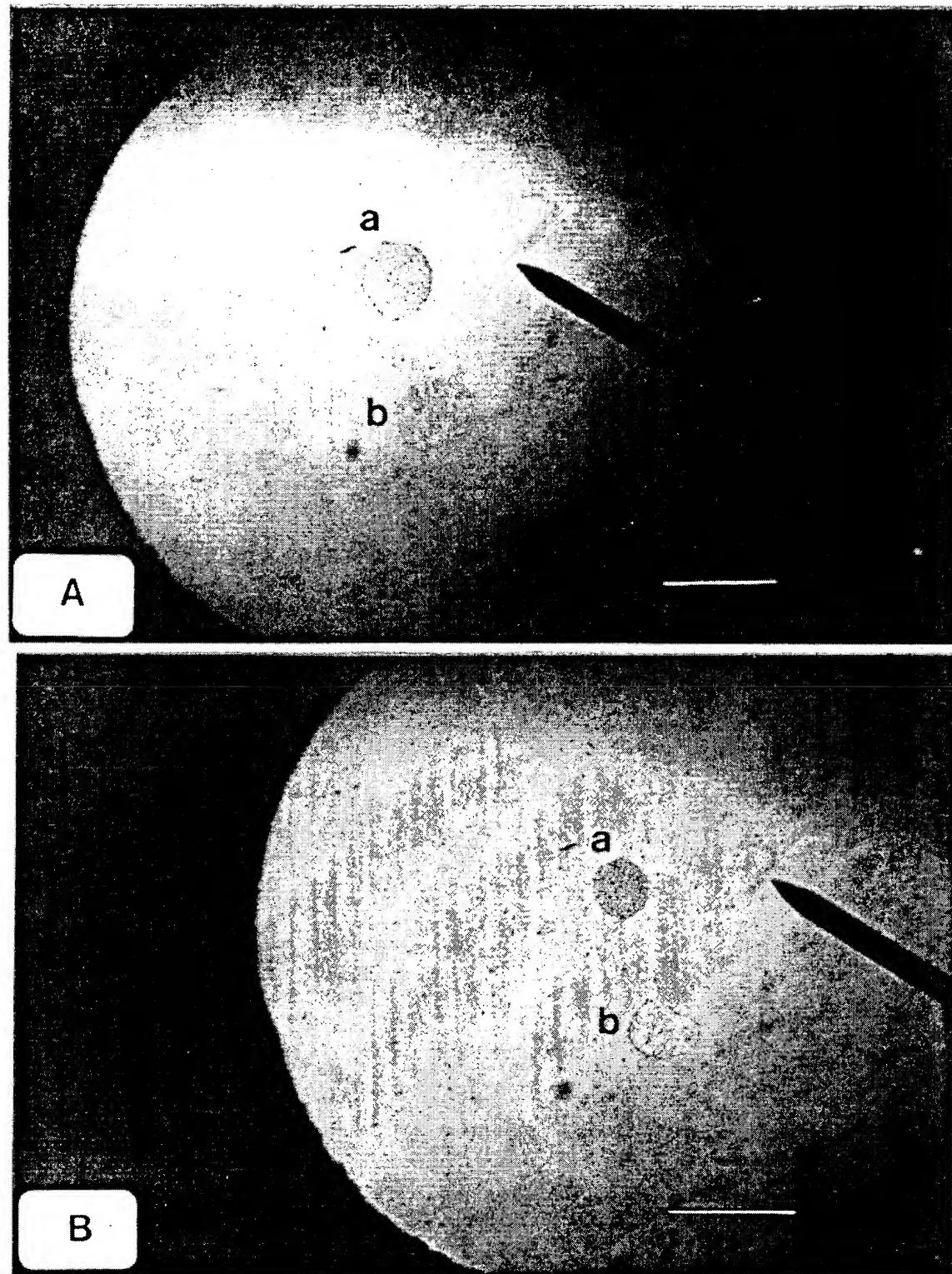


FIG. 8.39

DEPARTMENT OF PHYSICS

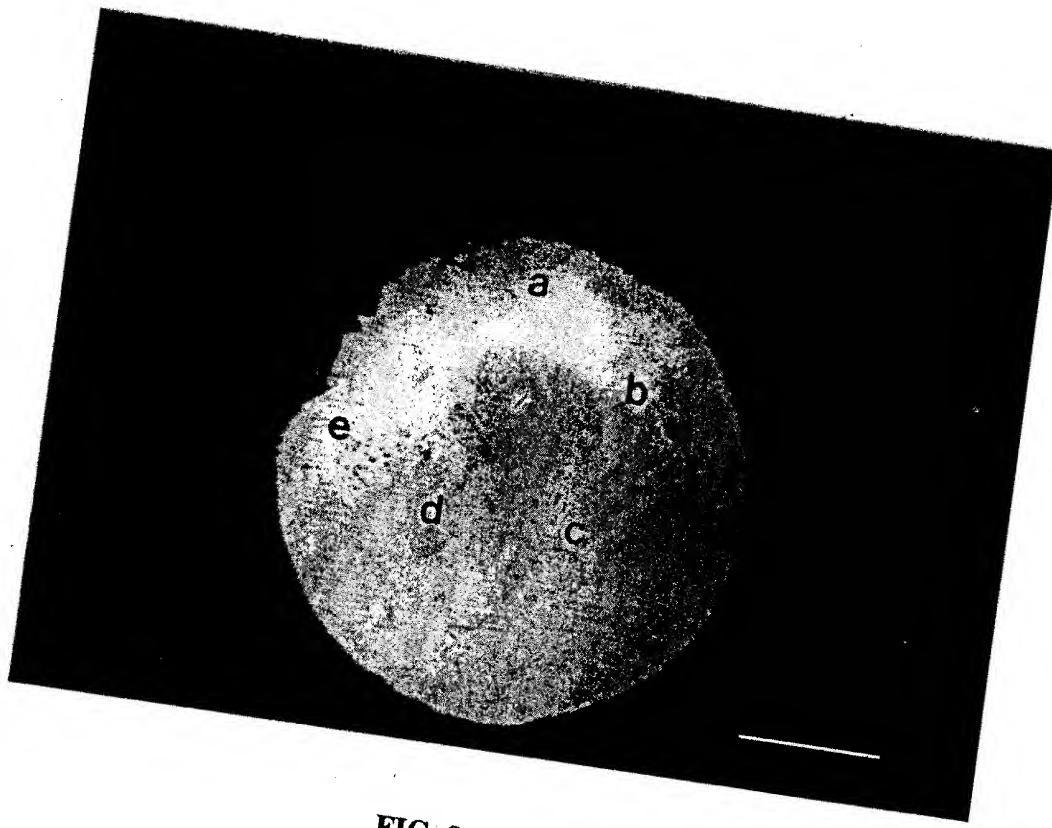


FIG. 8.40

09826296 " 06204

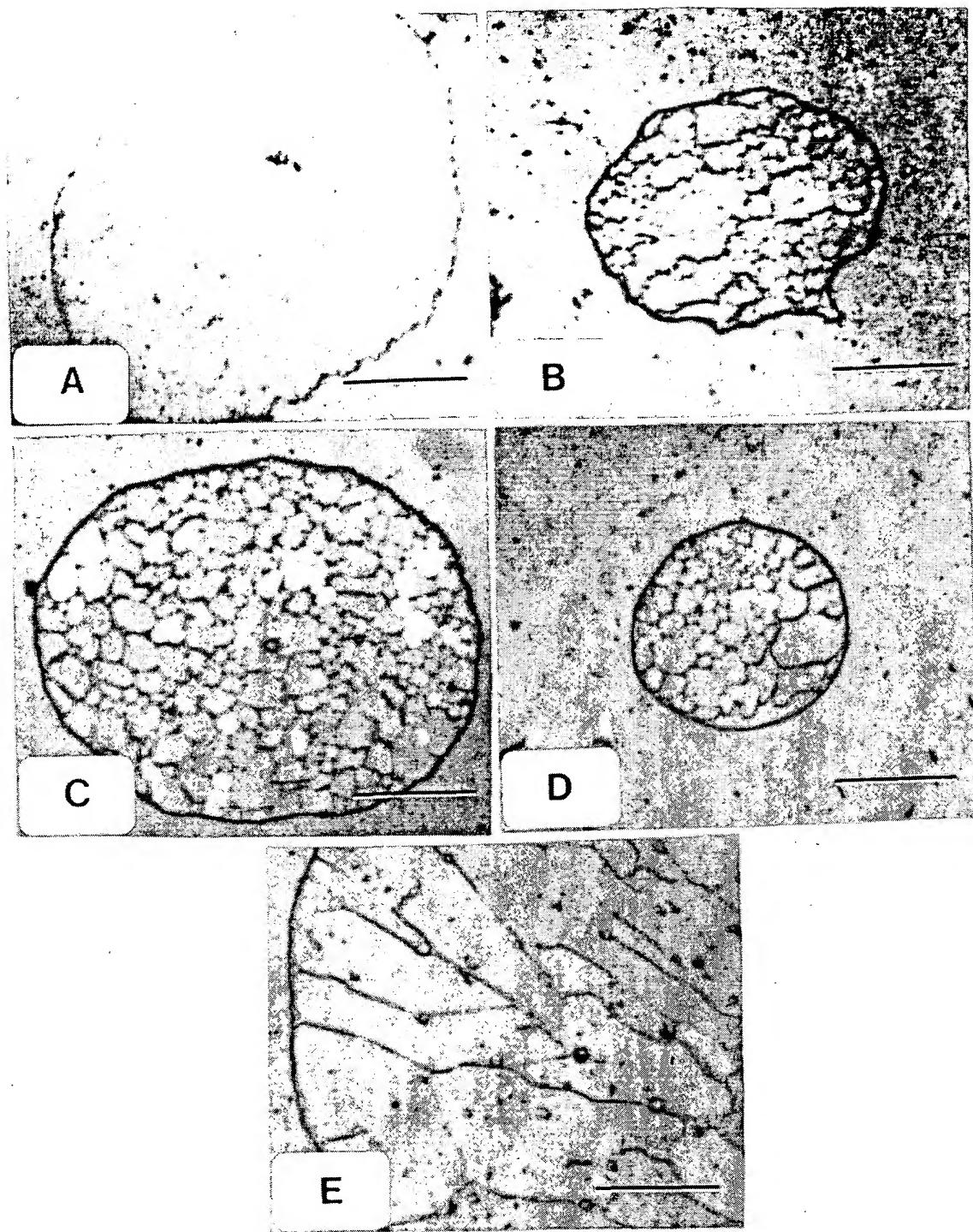


FIG. 8.41

09676296 - 060704

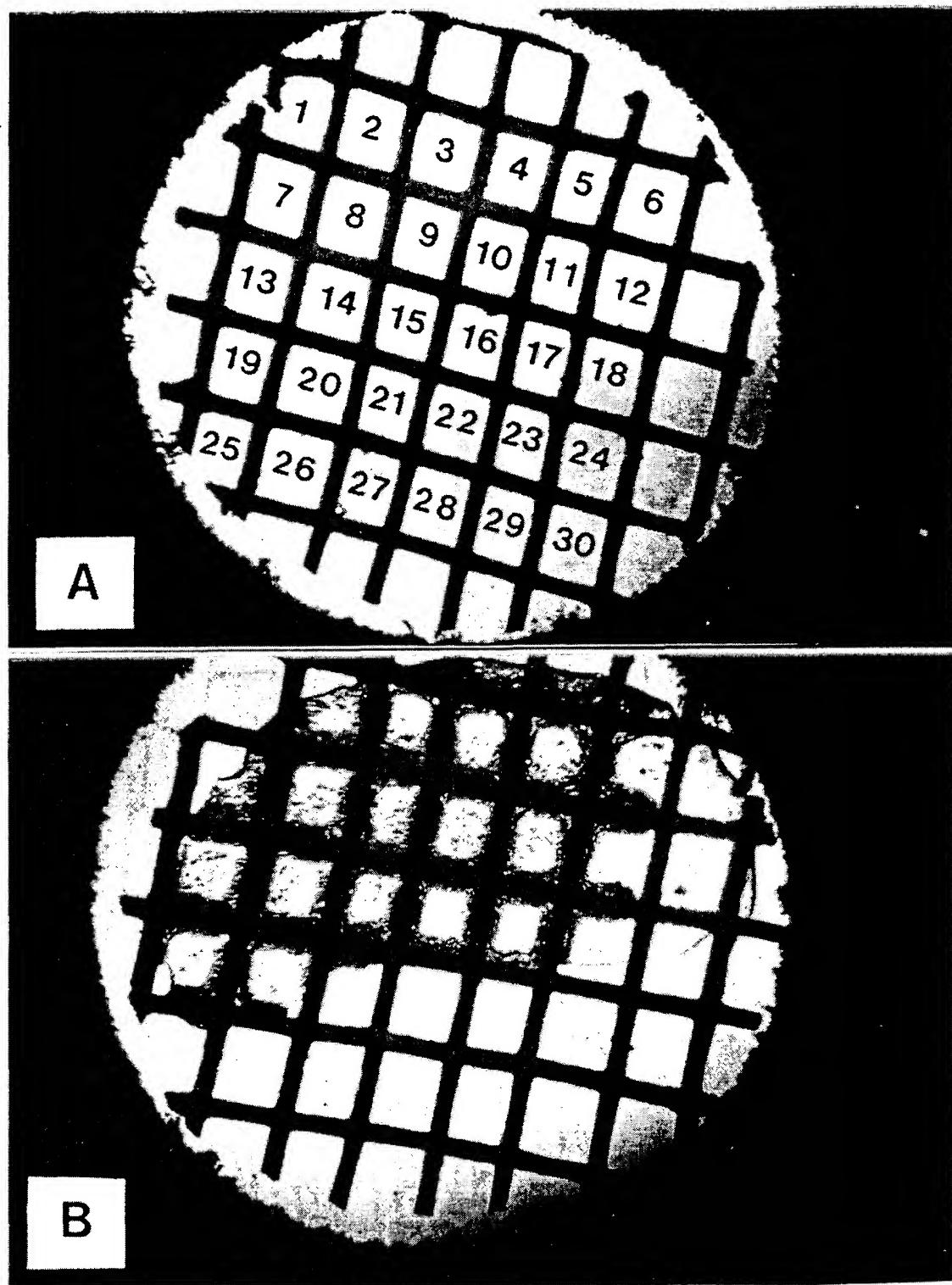


FIG. 8.42

DNA sequence of Tm 13.17 cDNA clone

B	E
a	C
m	O
H	R
I	I

1 AGTGGATCCAAAGAATTGGCACGAGACTACTAACGATCAAGTTGCTCTGTTGTCTAATCT  
M K L L C C L I S

61 CCCTCATTCTGTTGGTCACAGTTCAGGCCCTGACCGAGGCACAAATTGAGAAACTGAACA  
L I L L V T V Q A L T E A Q I E K L N K ↑

121 AGATCAGCAAAAATGTCAAAATGAAAGTGGAGTGTCCCAAGAGATCATAACCAAAGCTC  
I S K K C Q N E S G V S Q E I I T K A R

181 GCAACGGTGACTGGGAGGACGATCCTAAACTGAAACGCCAAGTTTTGCGTGGCCAGGA  
N G D W E D D P K L K R Q V F C V A R N

241 ACGCCGGTCTGGCCACGGAACTGGGAGAGGTGGTGGTCGACGTGTTGAGGGAGAAGGTGA  
A G L A T E S G E V V V D V L R E K V R

301 GGAAGGTCACTGACAACGACGAAGAAACTGAGAAAATCATCAATAAGTGCGCCGTCAAGA  
K V T D N D E E T E K I I N K C A V K R

361 GAGATACTGTAAGAGAGACGGTGTTCAATAACTTTCAAATGTGTCAGAAAAACAAGCCAA  
D T V E E T V F N T F K C V M K N K P K

421 AGTTCTCACCAAGTGTGATTGAACCACCACGACTAGTAGATGGTCAAATGGTGTGCTTAC  
F S P V D \* X  
h o i

481 ATATAAAAATAAAGTGTTCTGTGATGTAAAAAAAAAAAAAAAAAAACTC  
 polyadenylation signal poly (A) tail (26)

537 AGAGTATTCTAGAGCGGCCGCGGCCATCGTTCCACCC

FIG. 8.43

1 GGCACGAGCAAAA AT GAAACTCCTCTTGTGCTTGC GTT CGCCGCC  
 M K L L L C F A F A A

47 ATCGTCATGGAGCTCAGGCTCTCACCGACGACAGATACAGAAA  
 I V I G A Q A L T D E Q I Q K ↑

92 AGGAACAAGATCAGCAAAGAACGCCAGCAGGTGTCCGGAGTGTCC  
 R N K I S K E C Q Q V S G V S

137 CAAGAGACGATCGACAAAGTCCGCACAGGTGTCTGGTCGATGAT  
 Q E T I D K V R T G V L V D D

182 CCCAAAATGAAGAACGACGTCCCTCTGCTTCTCGAAGAAAATGGA  
 P K M K H V L C F S K K T G

226 GTGGCAACCGAACGCCGGAGACACCAATGTGGAGGTACTCAAAGCC  
 V A T E A G D T N V E V L K A

271 AAGCTGAAGCATGTGGCCAGCGACGAAGAGGGTGGACAAGATCGTG  
 K L K H V A S D E E V D K I V

316 CAGAAGTGC GTGGTCAAGAACGCCACACCAAGAGGAAACGGCTTAT  
 Q K C V V K A T P E E T A Y

361 GACACCTTCAAGTGTATTTACGACAGCAACCTGATTCTCTCC  
 D T F K C I Y D S K P D F S P

406 ATTGATTAATTGTTTGTATTTGACTGAATTGACAATAAGGT  
 I D \*

polyadenylation signal

451 ACTATCGTTATGTAAAAAAAAAAAAAA

poly (A) tail

FIG. 8.44